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183494

From: Seharaseyon, Jegatheesan  
Sent: Tuesday, March 28, 2006 4:06 PM  
To: STIC-Biotech/ChemLib  
Subject: Re:10/067832

Please search SEQ ID NO: 14 of 10/067832.

Thanks,

Seyon.

J.Seharaseyon  
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STIC  
183494  
03/28/06

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Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 29, 2006, 09:01:25 ; Search time 79 Seconds  
(without alignments)  
183.538 Million cell updates/sec

Title: US-10-067-832D-14  
Perfect score: 164  
Sequence: 1 MIEVVDRLGKVKVKNVTDITGLKLLIAA 33

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	163	99.4	33	2	AAY08414 Human bea
2	163	99.4	33	8	ADR43346 Human Bea
3	163	99.4	73	2	AAY08413 P. obesu
4	163	99.4	73	3	AAB36290 Iersaeli s
5	163	99.4	73	4	AAM39680 Human pol
6	163	99.4	89	4	AAM41466 Human pol
7	163	99.4	115	5	ABP41331 Human ova
8	152	92.7	73	4	ABBS5910 Drosophil
9	147.5	89.9	32	3	AAB36291 Human bea
10	146	89.0	73	3	AAG40885 Zea mays
11	146	89.0	73	3	AAG41925 Arabidops
12	146	89.0	96	3	AAG41924 Arabidops
13	141	86.0	73	3	AAG27281 Zea mays
14	130.5	79.6	73	8	ADT58384 Plant pol
15	114	69.5	32	9	ADV95409 Yeast ubi
16	114	69.5	40	9	ADV95411 Yeast ubi
17	114	69.5	89	5	ADH32312 Novel yea
18	114	69.5	320	6	ABR83620 HUB1-Gfp
19	68	41.5	27	4	AAM21187 Peptide #
20	68	41.5	27	4	ABB43508 Peptide #
21	68	41.5	27	4	AAM37402 Peptide #
22	68	41.5	27	4	ABB26468 Protein #
23	68	41.5	27	4	AAM77251 Human bon
24	68	41.5	27	4	AAM64443 Human bra

25	68	41.5	27	5	ABG46267 Human pep
26	56.5	34.5	282	2	AAR34706 NAD cyc1a
27	56.5	34.5	282	2	AAR70095 NAD cyc1a
28	56.5	34.5	282	2	Aaw80290 Aplysia c
29	54.5	33.2	169	8	ADX73119 Plant ful
30	54	32.9	525	6	ADA48272 Rice prot
31	54	32.9	525	7	ADC07784 Rice prot
32	53.5	32.6	1186	5	ABB93602 Herbicida
33	52.5	32.0	630	4	ABB61655 Drosophil
34	52.5	32.0	831	5	ABG91571 Purine/py
35	52	31.7	231	7	ADC95674 E. faeciu
36	52	31.7	1094	3	AAB23858 Haemophil
37	51	31.1	37	6	ABU61308 Human A d
38	51	31.1	37	8	ADP21530 Human LDL
39	51	31.1	527	7	ADE07959 Novel pro
40	51	31.1	527	8	ADO47164 Amino aci
41	51	31.1	527	8	ADP12444 Protein e
42	51	31.1	527	9	ADW47997 Recombina
43	51	31.1	3197	7	ABM85418 Mouse pro
44	51	31.1	4183	7	ABM85419 Human pro
45	51	31.1	4419	8	ADN11590 Human C99

ALIGNMENTS

RESULT 1  
AAY08414  
ID AAY08414 standard; protein; 33 AA.  
XX  
AC AAY08414;  
XX  
DT 24-JUL-1999 (first entry)  
XX  
DE Human beacon protein.  
XX  
KW Beacon; hypothalamus; obese; lean; agonist; antagonist; treatment;  
KW obesity; anorexia; weight maintenance; energy imbalance; diabetes;  
KW metabolic syndrome; dyslipidemia; hypertension; insulin resistance;  
KW medicament; livestock; diagnosis; human.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 15 /label= unknown  
FT /note= "encoded by CNC"  
XX  
PN WO9923217-A1.

XX  
14-MAY-1999.  
XX  
30-OCT-1998; 98WO-AU000902.  
XX  
31-OCT-1997; 97AU-00000117.  
XX  
11-NOV-1997; 97AU-00000323.  
XX  
(ITDI-) INT DIABETES INST.  
XX  
(UYDB-) UNIV DEAKIN.  
XX  
Zimmet PZ, Collier G;  
XX  
WPI; 1999-337484/28.  
XX  
N-PSDB; AAX57370.  
XX  
New gene encoding a beacon protein associated with modulation of obesity,  
XX  
diabetes and metabolic energy levels.  
XX  
Claim 2; Page 54; 85pp; English.  
XX  
This invention describes a novel beacon protein and its encoding nucleic  
XX  
acid which is expressed in larger amounts in hypothalamus tissue of obese  
XX  
animals compared to lean animals. Agonists and antagonists of beacon can

CC be used to treat obesity, anorexia, weight maintenance, energy imbalance,  
 CC diabetes, metabolic syndrome, dyslipidemia, hypertension and/or insulin  
 CC resistance. The beacon protein, itself is used to manufacture medicaments  
 CC for treatment of obesity, anorexia, energy imbalance or diabetes. The  
 CC treatment is contemplated for both human and animals, such as those  
 CC important to the livestock industry. The antibody and polynucleotides are  
 CC useful in diagnosis of conditions as above

XX Sequence 33 AA;

Query Match 99.4%; Score 163; DB 2; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 9.6e-15;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIEVNCNDRLGKVKVVKCNTDDTIGDLKLLIAA 33

DB 1 MIEVNCNDRLGKVKVVKCNTDDTIGDLKLLIAA 33

RESULT 2  
 ADR43346

ID ADR43346 standard; peptide; 33 AA.

XX ADR43346;

DT 04-NOV-2004 (first entry)

DE Human Beacon protein.

XX Beacon; Anorectic; Anabolic; Antidiabetic; Cytostatic; Cardiant;  
 KW Antinflammatory; Immunosuppressive; Antinfertility; Neuroprotective;  
 KW Nootropic; CLK; myopathy; obesity; anorexia; diabetes; cancer;  
 KW heart disease; inflammation; Alzheimer's; Parkinson's; Pearson Syndrome;  
 KW Pyruvate Carboxylase Deficiency; Pyruvate Dehydrogenase Deficiency;  
 KW Cancer; Acoustic Neuroma; Acute Lymphocytic Leukemia; Carcinoma;  
 KW Leukemia.

XX Homo sapiens.

XX WO2004069866-A1.

XX 19-AUG-2004.

XX 10-FEB-2004; 2004WO-AU000147.

XX 10-FEB-2003; 2003US-0446191P.

XX (AUTO-) AUTOGEN RES PTY LTD.

PA (UYDE-) UNIV DEAKIN.

XX Collier G, Walder K, Kerr-Bayles L;

XX WPI; 2004-604412/58.

XX New isolated ligands of mammalian or avian Beacon, useful for e.g.  
 PT preventing or treating disorders associated with myopathy, obesity,  
 PT diabetes, cancer, heart disease, inflammation, or disorders associated  
 PT with the immune system.

PS Claim 3; SEQ ID NO 4; 194pp; English.

XX The present invention relates to an isolated ligand of mammalian or avian  
 CC Beacon or a homolog or derivative of the Beacon. The composition  
 CC (including the agent capable of modulating the interaction between a  
 CC Beacon and a CLK) or methods are useful for manufacturing a medicament  
 CC for the treatment of a condition characterized by a healthy or unhealthy  
 CC state, including the presence or absence of a disorder associated with  
 CC myopathy, obesity, anorexia, weight maintenance, diabetes, disorders  
 CC associated with mitochondrial dysfunction, genetic disorders, cancer,  
 CC heart disease, inflammation, disorders associated with the immune system,  
 CC infertility, disease associated with the brain and/or metabolic energy  
 CC levels. The disease is selected from Alzheimer's, Parkinson's, diabetes,  
 CC autism, and the aging process, LIC (Lethal Infantile Cardiomyopathy),

CC abgr;-oxidation Defects, COX Deficiency, Mitochondrial Cytopathy, Alper's  
 CC Disease, Barth Syndrome, Carnitine-Acyl-Carnitine Deficiency, Carnitine  
 CC Deficiency, Co-Enzyme Q10 Deficiency, Complex I Deficiency, Complex II  
 CC Deficiency, Complex III Deficiency, Complex IV Deficiency, Complex V  
 CC Deficiency, chronic progressive external ophthalmoplegia syndrome (CPEO),  
 CC CPT I Deficiency, Glutaric Aciduria Type II, Kearns-Sayre syndrome (KSS),  
 CC lactic acidosis, long-chain acyl-CoA dehydrogenase deficiency (LCAD),  
 CC LCHAD, Leigh Disease, Leber Hereditary Optic Neuropathy (LHON), Luft  
 CC Disease, mitochondrial DNA depletion, Mitochondrial Encephalopathy,  
 CC Pearson Syndrome, Pyruvate Carboxylase Deficiency, Pyruvate Dehydrogenase  
 CC Deficiency, and the other diseases mentioned in the specification. The  
 CC cancer is selected from ABLI protooncogene, AIDS Related Cancers,  
 CC Acoustic Neuroma, Acute Lymphocytic Leukemia, Acute Myeloid Leukemia,  
 CC Adenocystic carcinoma, Adrenocortical Cancer, Agnogenic myeloid  
 CC metaplasia, Alopecia, Alveolar soft-part sarcoma, Anal cancer,  
 CC Angiosarcoma, Aplastic Anemia, Astrocytoma, Ataxia-telangiectasia, Basal  
 CC Cell Carcinoma (Skin), Bladder Cancer, Bone Cancer, Bowel cancer, Brain  
 CC Stem Glioma, Brain and CNS Tumours, Breast Cancer, Childhood Cancer,  
 CC Tumours, Cervical Cancer, Childhood Brain Tumour, Childhood Cancer,  
 CC Childhood Leukemia, and other cancers mentioned in the specification. The  
 CC 11 sequences mentioned in the body of the specification do not correspond  
 CC to the sequences represented in the SEQ ID listing.

XX Sequence 33 AA;

Query Match 99.4%; Score 163; DB 8; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 9.6e-15;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIEVNCNDRLGKVKVVKCNTDDTIGDLKLLIAA 33

DB 1 MIEVNCNDRLGKVKVVKCNTDDTIGDLKLLIAA 33

RESULT 3

AA08413

ID AAY08413 standard; protein; 73 AA.

XX AC AAY08413;

DT 24-JUL-1999 (first entry)

DE P. obeaus beacon protein.

XX Beacon; hypothalamus; obese; lean; agonist; antagonist; treatment;  
 KW obesity; anorexia; weight maintenance; energy imbalance; diabetes;  
 KW metabolic syndrome; dyslipidemia; hypertension; insulin resistance;  
 KW medicament; livestock; diagnosis.

XX Psammomys obesus.

XX WO9923217-A1.

XX 14-MAY-1999.

XX 30-OCT-1998; 98WO-AU000902.

XX 31-OCT-1997; 97AU-00000117.

XX 11-NOV-1997; 97AU-00000323.

XX (ITDI-) INT DIABETES INST.

XX (UYDE-) UNIV DEAKIN.

XX Zimmet PZ, Collier G;

XX WPI; 1999-337484/28.

XX N-PSDB; AAX57359.

XX New gene encoding a beacon protein associated with modulation of obesity,  
 PT diabetes and metabolic energy levels.

PS Claim 2; Page 50; 85pp; English.

CC This invention describes a novel beacon protein and its encoding nucleic  
 CC acid which is expressed in larger amounts in hypothalamus tissue of obese  
 CC animals compared to lean animals. Agonists and antagonists of beacon can  
 CC be used to treat obesity, anorexia, weight maintenance, energy imbalance,  
 CC diabetes, metabolic syndrome, dyslipidemia, hypertension and/or insulin  
 CC resistance. The beacon protein, itself is used to manufacture medicaments  
 CC for treatment of obesity, anorexia, energy imbalance or diabetes. The  
 CC treatment is contemplated for both human and animals, such as those  
 CC important to the livestock industry. The antibody and polynucleotides are  
 CC useful in diagnosis of conditions as above  
 XX  
 SQ Sequence 73 AA;

Query Match 99.4%; Score 163; DB 2; Length 73;

Best Local Similarity 97.0%; Pred. No. 2.2e-14;  
 Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKKVVKCMTDDTIGDLKLLIAA 33

Db 1 MIEVVCNDRLGKKVVKCMTDDTIGDLKLLIAA 33

RESULT 4

AAB36290  
 ID AAB36290 standard; protein; 73 AA.

XX AC AAB36290;

XX DT 23-FEB-2001 (first entry)

XX DE Israeli sand rat beacon ligand.

XX KW Israeli sand rat; beacon; obesity; NIDDM; energy balance; diabetes;  
 KW ligand.

XX OS Psammomys obesus.

XX PN WO20064931-A1.

XX PD 02-NOV-2000.

XX PF 19-APR-2000; 2000WO-AU000342.

XX PR 23-APR-1999; 99AU-00009919.

XX PR 24-MAR-2000; 2000AU-00006454.

XX PA (AUTO-) AUTOGEN PTY LTD.

XX PI Collier G, Walder K, Zimmet P;

XX PT WPI; 2000-687311/67.

XX DR N-PSDB; AAC81767.

XX PT Ligand of beacon protein useful for treating obesity, anorexia, energy  
 PT imbalance, diabetes, metabolic syndrome, dyslipidemia, hypertension and  
 PT insulin resistance.

XX PS Claim 3; Fig 1; 67pp; English.

XX CC The present invention is related to the isolation of a ligand known as  
 CC beacon from the Israeli sand rat. Beacon is associated with the  
 CC regulation of energy balance, and the protein, its coding sequence and  
 CC analogues can be used in the treatment of diabetes, obesity, anorexia,  
 CC energy imbalance, metabolic syndrome, dyslipidaemia, hypertension and  
 CC insulin resistance. In addition, they can be used in agriculture to  
 CC produce leaner animals

XX SQ Sequence 73 AA;

Query Match 99.4%; Score 163; DB 3; Length 73;

Best Local Similarity 97.0%; Pred. No. 2.2e-14;  
 Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKKVVKCMTDDTIGDLKLLIAA 33  
 Db 1 MIEVVCNDRLGKKVVKCMTDDTIGDLKLLIAA 33

RESULT 5

AAM39680  
 ID AAM39680 standard; protein; 73 AA.

XX AC AAM39680;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 2825.

XX KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukaemia.

XX OS Homo sapiens.

XX PN WO200153312-A1.

XX PD 26-JUL-2001.

XX PF 26-DEC-2000; 2000WO-US034263.

XX PR 23-DEC-1999; 99US-00471275.

XX PR 21-JAN-2000; 2000US-00488725.

XX PR 25-APR-2000; 2000US-00552317.

XX PR 20-JUN-2000; 2000US-00598042.

XX PR 19-JUL-2000; 2000US-00620312.

XX PR 03-AUG-2000; 2000US-00653450.

XX PR 14-SEP-2000; 2000US-00662131.

XX PR 19-OCT-2000; 2000US-00693036.

XX PR 29-NOV-2000; 2000US-00727344.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

XX PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;

XX PI Zhou P, Goodrich R, Drmanac RT;

XX DR WPI; 2001-442253/47.

XX DR N-PSDB; AAI58836.

XX PT Novel nucleic acids and polypeptides, useful for treating disorders such  
 PT as central nervous system injuries.

XX PS Example 4; SEQ ID NO 2825; 10078pp; English.

XX CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the  
 CC encoded polypeptides (AAM38642-AA42213) with nootropic,  
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localised neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemia and  
 CC C.N.S disorders. Note: The sequence data for this patent did not form  
 CC part of the printed specification

XX SQ Sequence 73 AA;

Query Match 99.4%; Score 163; DB 4; Length 73;



CC respiratory disorders, neurological disorders, gastrointestinal disorders  
CC and urinary system disorders. Ovarian antigen polypeptides and  
CC polynucleotides may also be used in screening for compounds which  
CC modulate ovarian antigen expression or activity. The polynucleotides may  
CC further be used for gene therapy, chromosome mapping, in the  
CC identification of individuals and in forensic analysis, and the  
CC polypeptides may be used as food additives or to prepare antibodies  
CC useful in disease diagnosis, drug targeting and phenotyping. The present  
CC sequence represents a human ovarian antigen of the invention. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 115 AA;

Query Match 99.4%; Score 163; DB 5; Length 115;  
Best Local Similarity 97.0%; Pred. No. 3.4e-14;  
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVVKCNTDDTIGDLKKLIAA 33  
DB 43 MIEVVCNDRLGKVKVVKCNTDDTIGDLKKLIAA 75

RESULT 8  
ID ABB59910 standard; protein; 73 AA.  
XX  
AC ABB59910;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Drosophila melanogaster polypeptide SEQ ID NO 6522.  
XX  
KW Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical.  
XX  
OS Drosophila melanogaster.  
XX  
PN WO200171042-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 23-MAR-2001; 2001WO-US009231.  
XX  
PR 23-MAR-2000; 2000US-0191637P.  
PR 11-JUL-2000; 2000US-00614150.  
XX  
PA (PEKE ) PE CORP NY.  
XX  
PI Venter JC, Adams M, Li PWD, Myers EW;  
XX  
DR WPI; 2001-656860/75.  
DR N-PSDB; ABL04013.  
XX  
PT New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signalling and cell-cell  
PT interactions.  
XX  
PS Disclosure; SEQ ID NO 6522; 21pp + Sequence Listing; English.  
XX

CC The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
CC ABB72072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 73 AA;

Query Match 92.7%; Score 152; DB 4; Length 73;  
Best Local Similarity 87.9%; Pred. No. 6.7e-13;  
Matches 29; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVVKCNTDDTIGDLKKLIAA 33  
DB 1 MIEITCNDRLGKVKVVKCNPDPTIGDLKKLIAA 33

RESULT 9  
ID AAB36291 standard; protein; 32 AA.  
XX  
AC AAB36291;  
XX  
DT 23-FEB-2001 (first entry)  
XX  
DE Human beacon (short form) protein sequence.  
XX  
KW Israeli sand rat; beacon; obesity; NIDDM; energy balance; diabetes;  
KW ligand; human.  
XX  
OS Homo sapiens.  
XX  
PN WO200064931-A1.  
XX  
PD 02-NOV-2000.  
XX  
PF 19-APR-2000; 2000WO-AU000342.  
XX  
PR 23-APR-1999; 99AU-00009919.  
PR 24-MAR-2000; 2000AU-00006454.  
XX  
PA (AUTO-) AUTOGEN PTY LTD.  
XX  
PI Collier G, Walder K, Zimmert P;  
XX  
DR WPI; 2000-687311/67.  
DR N-PSDB; AAC81770.  
XX  
PT Ligand of beacon protein useful for treating obesity, anorexia, energy  
PT imbalance, diabetes, metabolic syndrome, dyslipidemia, hypertension and  
PT insulin resistance.  
XX  
PS Disclosure; Fig 1B; 67pp; English.  
XX  
CC The present invention is related to the isolation of a ligand known as  
CC beacon from the Israeli sand rat. Beacon is associated with the  
CC regulation of energy balance, and the protein, its coding sequence and  
CC analogues can be used in the treatment of diabetes, obesity, anorexia,  
CC energy imbalance, metabolic syndrome, dyslipidemia, hypertension and  
CC insulin resistance. In addition, they can be used in agriculture to  
CC produce leaner animals  
XX  
SQ Sequence 32 AA;

Query Match 89.9%; Score 147.5; DB 3; Length 32;  
Best Local Similarity 97.0%; Pred. No. 1.2e-12;  
Matches 32; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MIEVVCNDRLGKVKVVKCNTDDTIGDLKKLIAA 33  
DB 1 MIEVVCNDRLGKVKVVKCNTDDTIGDL-KLIAA 32

RESULT 10  
ID AAG40885 standard; protein; 73 AA.  
XX  
AC AAG40885;  
XX  
DT 18-OCT-2000 (first entry)

XX Zea mays protein fragment SEQ ID NO: 50790.  
DE  
XX  
KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridization assay; genetic mapping; gene expression control; promoter;  
XX termination sequence; corn.  
OS  
XX Zea mays subsp. mays.  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
XX 25-FEB-2000; 2000EP-00301439.  
XX  
PR 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127462P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
PR 23-APR-1999; 99US-0130891P.  
PR 28-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
PR 30-APR-1999; 99US-0132407P.  
PR 04-MAY-1999; 99US-0132484P.  
PR 05-MAY-1999; 99US-0132485P.  
PR 06-MAY-1999; 99US-0132486P.  
PR 07-MAY-1999; 99US-0132487P.  
PR 11-MAY-1999; 99US-0132566P.  
PR 14-MAY-1999; 99US-0134218P.  
PR 14-MAY-1999; 99US-0134219P.  
PR 14-MAY-1999; 99US-0134221P.  
PR 14-MAY-1999; 99US-0134370P.  
PR 18-MAY-1999; 99US-0134768P.  
PR 19-MAY-1999; 99US-0134941P.  
PR 20-MAY-1999; 99US-0135124P.  
PR 21-MAY-1999; 99US-0135353P.  
PR 24-MAY-1999; 99US-0135629P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 01-JUN-1999; 99US-0136782P.  
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RESULT 14
ADT58384
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XX
AC ADT58384;
XX
DT 13-JAN-2005 (first entry)
XX
DE Plant polypeptide, SEQ ID 8461.
XX
KW Plant; transgenic; cold tolerance; growth rate; drought tolerance;
KW disease resistance; galactomannan production; plant growth regulator;
KW heat tolerance; herbicide tolerance; lignin production;
KW extreme osmotic condition tolerance; pathogens resistance;
KW pest resistance; yield improvement; seed oil yield; seed protein yield.
XX
OS Viridiplantae.
XX
PN US2004216190-A1.
XX
PD 28-OCT-2004.
XX
PF 18-DEC-2003; 2003US-00739930.
XX
PR 28-APR-2003; 2003US-00424599.
PR 28-APR-2003; 2003US-00425115.
XX
PA (KOVA/) KOVALIC D K.
XX
PI Kovalic DK;
XX
DR WPI; 2004-757369/74.
XX
PT New recombinant DNA constructs useful in the field of biochemistry and
  genetics, and in particular for producing transgenic plants with improved
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biological characteristics.

Claim 2; SEQ ID NO 8461; 14pp; English.

The invention relates a recombinant DNA construct comprising a polynucleotide having any of 5544 nucleotide sequences (CDNs SEQ ID NO: 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean, Arabidopsis, wheat and rape but the specification does not indicate which sequences is derived from which organism. Also included is a method of producing a plant having an improved property, comprising transforming a plant with a recombinant DNA construct comprising a promoter region functional in a plant cell operably joined to a polynucleotide encoding a polypeptide associated with the property, and growing the transformed plant. The property is selected from improving plant cold tolerance, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for improving plant drought tolerance, for providing increased resistance to plant diseases, for galactomanan production, for production of plant growth regulators, for improving plant heat tolerance, for improving plant tolerance to herbicides, for increasing the rate of homologous recombination in plants, for lignin production, for improving plant tolerance to extreme osmotic conditions, for improving plant tolerance to pathogens or pests, for yield improvement by modification of photosynthesis, for modifying seed oil yield and/or content, for modifying seed protein yield and/or content, for yield improvement by modification of carbohydrate, nitrogen or phosphorus use and/or uptake and for yield improvement by providing improved plant growth and development under at least one stress condition. The polynucleotide may also encode a plant transcription factor. The methods and compositions of the present invention are useful in the field of biochemistry and genetics, in particular for producing transgenic plants with improved biological characteristics such as increased yield, improved nitrogen flow, increasing plant tolerance to cold or heat, improving plant tolerance to extreme osmotic and drought conditions, and improving plant tolerance to plant pests or pathogens. They can also be used in physical arrays of molecules, plant breeding markers, computer-based storage and analysis systems. The present sequence is one of the 5544 plant protein sequences of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20040216190.

Sequence 73 AA;

Query Match 79.6%; Score 130.5; DB 8; Length 73;  
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RESULT 15  
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AC ADV95409;  
XX XX  
DT 07-APR-2005 (first entry)  
XX XX  
DE Yeast ubiquitin like protein Hub1 amino terminal domain 1.  
XX XX  
KW Fusion protein; protein folding; protein structure;  
ubiquitin like protein.  
XX XX  
OS Saccharomyces cerevisiae.  
XX XX  
PN W02005003313-A2.  
XX XX  
PD 13-JAN-2005.  
XX PF  
28-JUN-2004; 2004WO-US020778.

Query Match 69.5%; Score 114; DB 9; Length 32;  
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Search completed: March 29, 2006, 09:03:17  
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Db 597 IKKNTDLDGDPFK 610

RESULT 8

AS3102

alpha-2-macroglobulin receptor precursor - chicken

NAlternate names: CD91; LDL receptor-related protein 1; low density lipoprotein receptor

CSpecies: Gallus gallus (chicken)

CDate: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 09-Jul-2004

CAccession: AS3102

RNimpf, J.; Stifani, S.; Bilous, P.T.; Schneider, W.J.

J. Biol. Chem. 269, 212-219, 1994

A>Title: The somatic cell-specific low density lipoprotein receptor-related protein of b

AReference number: AS3102; MUID:94103212; PMID:7506255

AAccession: AS3102

AStatus: preliminary

A.Molecule type: mRNA

A.Residues: 1-4543 <NIM>

A.Cross-references: UNIPROT:P98157; UNIPARC:UPI000013C4B3; GB:X74904; NID:g438006; PIDN;

C.Complex: The alpha-2-macroglobulin receptor complex consists of noncovalently-associated

d protein.

C.Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding

C.Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; calcium binding; glycopro

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F.29-56/Domain: LDL receptor ligand-binding repeat homology <LDL1>

F.117-110/Domain: LDL receptor ligand-binding repeat homology <LDL2>

F.1156-190/Domain: EGF homology <EG1>

F.156-190/Domain: EGF homology <EG2>

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F.480-521/Domain: EGF homology <EG3>

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F.168,2995/Modified site: erythro-beta-hydroxyasparagine (Aen) #status predicted

F.2955/Modified site: erythro-beta-hydroxyaspartic acid (Aap) #status predicted

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RESULT 9

T31652

hypothetical protein Y57A10A.aa - Caenorhabditis elegans

CSpecies: Caenorhabditis elegans

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A;Molecule type: DNA  
A;Residues: 1-201 <WIL>  
A;Cross-references: UNIPARC:UPI000007B48B; EMBL:AL117195; PIDN:CAB55035.1; CESP:Y57A10A.  
A;Experimental source: clone Y57A10A  
C;Genetics:  
A;Gene: CESP:Y57A10A.oe  
A;Introns: 152/2  
C;Superfamily: translation initiation factor eIF-4E

Query Match 31.4%; Score 51.5; DB 2; Length 201;  
Best Local Similarity 46.2%; Pred. No. 16;  
Matches 18; Conservative 5; Mismatches 7; Indels 9; Gaps 4;

QY 4 VVCNDR-LGKKVXV---KNTDPT---IGDL--KKLIAA 33  
DB 124 LVCNVRGGGSKSVWTKNCNDDDTNMRIGVLKSLMAA 162

RESULT 10

S42512  
recombination-activating protein RAG-2 - rabbit  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
A;Accession: S42512; S42513; S42515; S42514  
R;Fuschlotti, P.; Harindranath, N.; Mage, R.G.; McCormack, W.T.; Dhanarajan, P.; Roux, K.  
Mol. Immunol. 30, 1021-1032, 1993  
A;Title: Recombination activating genes-1 and -2 of the rabbit: cloning and characterization  
A;Reference number: S42511; MUID:93354283; PMID:8350872  
A;Accession: S42512  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-527 <FUS>  
A;Cross-references: UNIPROT:P34089; UNIPARC:UPI000013308B; EMBL:W77667; NID:g165685; PIDN:AAA03028.1; PI  
A;Accession: S42513  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-11,'1',13-15 <FU2>  
A;Cross-references: UNIPARC:UPI000016CSB2; EMBL:M99310; NID:g165683; PIDN:AAA03028.1; PI  
A;Accession: S42515  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 5-11,'1',13-113,'R',115-169,'K',171-350,'S',352-439,'R',441-527 <FU3>  
A;Cross-references: UNIPARC:UPI000016CSB1; EMBL:M99312; NID:g165681; PIDN:AAA03027.1; PI  
A;Accession: S42514  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 5-11,'1',13-164,'S',166-324,'R',326-350,'S',352-527 <FU4>  
A;Cross-references: UNIPARC:UPI000016CSB3; EMBL:M99311; NID:g165679; PIDN:AAA03026.1; PI  
C;Comment: This protein is required for immunoglobulin or T-cell receptor gene rearrange  
C;Superfamily: recombination-activating protein RAG-2

Query Match 31.1%; Score 51; DB 2; Length 527;  
Best Local Similarity 37.0%; Pred. No. 44;  
Matches 10; Conservative 6; Mismatches 9; Indels 2; Gaps 1;

QY 1 MIEVVCNDRLGKKVXVKCNTDPTIGDL 27  
DB 109 VMSVVCKN--NKKVTFRCRTDLVGDV 133

RESULT 11

T01857  
hypothetical protein F9D12.1 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 26-Feb-1999 #sequence\_revision 26-Feb-1999 #text\_change 09-Jul-2004  
A;Accession: T01857

R;Murray, J.; Langston, Y.; Ahrens, C.  
submitted to the EMBL Data Library, July 1998  
A;Description: The sequence of Arabidopsis thaliana F9D12.  
A;Reference number: Z14444  
A;Accession: T01857  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-662 <MUR>  
A;Cross-references: UNIPROT:O81505; UNIPARC:UPI00000A7B91; EMBL:AF077407; NID:g3319339;  
A;Experimental source: cultivar Columbia  
C;Genetics:  
A;Map position: 4  
A;Introns: 63/1, 102/3, 126/2, 165/3, 194/3, 223/3, 249/2, 315/3, 362/1  
A;Note: F9D12.1

Query Match 31.1%; Score 51; DB 2; Length 662;  
Best Local Similarity 39.1%; Pred. No. 53;  
Matches 9; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 9 RLGGKKVXVKCNTDPTIGDLKKLI 31  
DB 222 RQEKIVFTCCDDKVDADIRLV 244

RESULT 12

T39553  
vacuolar protein sorting-associated protein - fission yeast (Schizosaccharomyces pombe)  
C;Species: Schizosaccharomyces pombe  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
A;Accession: T39553  
R;Purnelle, B.; Goffeau, A.; Wood, V.; Lyne, M.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, February 1998  
A;Reference number: Z21863  
A;Accession: T39553  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-3131 <PUR>  
A;Cross-references: UNIPROT:O42926; UNIPARC:UPI000006AD1B; EMBL:AL021767; PIDN:CAA16910.  
A;Experimental source: strain 972h-; cosmid c16C6  
C;Genetics:  
A;Gene: SPDB:SPBC16C6.02c  
A;Map position: 2  
A;Introns: 8/1, 45/3, 96/3, 2958/3

Query Match 31.1%; Score 51; DB 2; Length 3131;  
Best Local Similarity 44.0%; Pred. No. 2e+02;  
Matches 11; Conservative 6; Mismatches 6; Indels 2; Gaps 1;

QY 1 MIEVVCNDRLGKKVX--VKCNTDPT 23  
DB 1873 VIEVVCNDRSGHRSQSVKIDPNET 1897

RESULT 13

S02392  
alpha-2-macroglobulin receptor precursor - human  
N;Alternate names: C991, LDL receptor-related protein 1; low density lipoprotein recepto  
C;Species: Homo sapiens (man)  
A;Accession: S02392; S30027; I37998; A39210; S12538  
R;Heiz, J.; Hamann, U.; Rogne, S.; Myklebost, O.; Gausepohl, H.; Stanley, K.K.  
EMBO J. 7, 4119-4127, 1988  
A;Title: Surface location and high affinity for calcium of a 500-kd liver membrane prote  
A;Reference number: S02392; MUID:89210795; PMID:3266596  
A;Accession: S02392  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-4544 <HER>  
A;Cross-references: UNIPROT:Q07954; UNIPARC:UPI0000055B03; EMBL:X13916; NID:g34338; PIDN  
R;Kristensen, T.  
submitted to the EMBL Data Library, October 1990  
A;Reference number: S30027  
A;Accession: S30027



QY 3 EVVNCNDRLGKKVXKCNCTDITGD 26  
 DB 3658 EFQCNTLCKPLAWKCGEDDCGD 3681

RESULT 14  
 S25111

Alpha-2-macroglobulin receptor precursor - mouse  
 N:Alternate names: CD91; LDL receptor-related protein 1; low density lipoprotein receptor  
 C:Species: Mus musculus (house mouse)  
 C:Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 09-Jul-2004  
 C:Accession: S25111; S32554  
 R:van Leuven, F.  
 submitted to the EMBL Data Library, July 1992  
 A:Reference number: S25111  
 A:Accession: S25111  
 A:Molecule type: mRNA  
 A:Residues: 1-4545 <VAN1>  
 A:Cross-references: UNIPROT:O61291; UNIPARC:UPI000002A148; EMBL:X67469; NID:G49941; PIDN  
 R:van Leuven, F.; Stas, L.; Raymakers, L.; Overbergh, L.; de Strooper, B.; Hilliker, C.;  
 Biochim. Biophys. Acta 1173, 71-74, 1993  
 A:Title: Molecular cloning and sequencing of the murine alpha-2-macroglobulin receptor c  
 A:Reference number: S32554; MUID:93250049; PMID:8485155  
 A:Accession: S32554  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-28;4416-4453 <VAN2>  
 A:Cross-references: UNIPARC:UPI0000173608; UNIPARC:UPI0000173609; EMBL:X67469  
 C:Complex: The alpha-2-macroglobulin receptor complex consists of noncovalently-associat  
 clated protein (see PIR:JX0281).  
 C:Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding  
 C:Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; calcium binding; glycopro  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-3944;3945-4545/Product: alpha-2-macroglobulin receptor #status predicted <MAT>  
 F:28-3944/Domain: alpha-2-macroglobulin receptor 515K chain #status predicted <515K>  
 F:720-65/Domain: LDL receptor ligand-binding repeat homology <LDL1>  
 F:73-109/Domain: LDL receptor ligand-binding repeat homology <LDL2>  
 F:116-149/Domain: EGF homology <EG1>  
 F:155-189/Domain: EGF homology <EG2>  
 F:199-240/Domain: LDL receptor YWTD-containing repeat homology <YW01>  
 F:241-282/Domain: LDL receptor YWTD-containing repeat homology <YW02>  
 F:293-335/Domain: LDL receptor YWTD-containing repeat homology <YW03>  
 F:336-379/Domain: LDL receptor YWTD-containing repeat homology <YW04>  
 F:380-421/Domain: LDL receptor YWTD-containing repeat homology <YW05>  
 F:422-469/Domain: LDL receptor YWTD-containing repeat homology <YW06>  
 F:479-520/Domain: EGF homology <EG3>  
 F:572-614/Domain: LDL receptor YWTD-containing repeat homology <YW07>  
 F:615-660/Domain: LDL receptor YWTD-containing repeat homology <YW08>  
 F:661-711/Domain: LDL receptor YWTD-containing repeat homology <YW09>  
 F:712-753/Domain: LDL receptor YWTD-containing repeat homology <YW10>  
 F:754-800/Domain: LDL receptor YWTD-containing repeat homology <YW11>  
 F:808-843/Domain: EGF homology <EG4>  
 F:855-891/Domain: LDL receptor ligand-binding repeat homology <LDL3>  
 F:896-932/Domain: LDL receptor ligand-binding repeat homology <LDL4>  
 F:937-979/Domain: LDL receptor ligand-binding repeat homology <LDL5>  
 F:977-1012/Domain: LDL receptor ligand-binding repeat homology <LDL6>  
 F:106-1052/Domain: LDL receptor ligand-binding repeat homology <LDL7>  
 F:1063-1098/Domain: LDL receptor ligand-binding repeat homology <LDL8>  
 F:1105-1141/Domain: LDL receptor ligand-binding repeat homology <LDL9>  
 F:1146-1183/Domain: LDL receptor ligand-binding repeat homology <LDL10>  
 F:1186-1222/Domain: EGF homology <EG5>  
 F:1228-1262/Domain: EGF homology <EG6>  
 F:1270-1309/Domain: LDL receptor YWTD-containing repeat homology <YW12>  
 F:1310-1356/Domain: LDL receptor YWTD-containing repeat homology <YW13>  
 F:1357-1399/Domain: LDL receptor YWTD-containing repeat homology <YW14>  
 F:1400-1446/Domain: LDL receptor YWTD-containing repeat homology <YW15>  
 F:1447-1489/Domain: LDL receptor YWTD-containing repeat homology <YW16>  
 F:1490-1532/Domain: LDL receptor YWTD-containing repeat homology <YW17>  
 F:1541-1579/Domain: EGF homology <EG7>  
 F:1584-1627/Domain: LDL receptor YWTD-containing repeat homology <YW18>  
 F:1628-1670/Domain: LDL receptor YWTD-containing repeat homology <YW19>  
 F:1671-1714/Domain: LDL receptor YWTD-containing repeat homology <YW20>

F:1715-1754/Domain: LDL receptor YWTD-containing repeat homology <YW21>  
 F:1755-1797/Domain: LDL receptor YWTD-containing repeat homology <YW22>  
 F:1798-1847/Domain: LDL receptor YWTD-containing repeat homology <YW23>  
 F:1851-1887/Domain: EGF homology <EG8>  
 F:1935-1977/Domain: LDL receptor YWTD-containing repeat homology <YW24>  
 F:1978-2020/Domain: LDL receptor YWTD-containing repeat homology <YW25>  
 F:2021-2064/Domain: LDL receptor YWTD-containing repeat homology <YW26>  
 F:2065-2106/Domain: LDL receptor YWTD-containing repeat homology <YW27>  
 F:2107-2152/Domain: LDL receptor YWTD-containing repeat homology <YW28>  
 F:2160-2195/Domain: EGF homology <EG9>  
 F:2200-2242/Domain: LDL receptor YWTD-containing repeat homology <YW29>  
 F:2254-2295/Domain: LDL receptor YWTD-containing repeat homology <YW30>  
 F:2345-2389/Domain: LDL receptor YWTD-containing repeat homology <YW31>  
 F:2390-2430/Domain: LDL receptor YWTD-containing repeat homology <YW32>  
 F:2431-2474/Domain: LDL receptor YWTD-containing repeat homology <YW33>  
 F:2483-2518/Domain: EGF homology <EG10>  
 F:2525-2562/Domain: LDL receptor ligand-binding repeat homology <LDLB>  
 F:2567-2601/Domain: LDL receptor ligand-binding repeat homology <LDLC>  
 F:2606-2640/Domain: LDL receptor ligand-binding repeat homology <LDLD>  
 F:2653-2689/Domain: LDL receptor ligand-binding repeat homology <LDLE>  
 F:2697-2731/Domain: LDL receptor ligand-binding repeat homology <LDLF>  
 F:2735-2770/Domain: LDL receptor ligand-binding repeat homology <LDLG>  
 F:2775-2813/Domain: LDL receptor ligand-binding repeat homology <LDLH>  
 F:2819-2854/Domain: LDL receptor ligand-binding repeat homology <LDLI>  
 F:2859-2898/Domain: LDL receptor ligand-binding repeat homology <LDLJ>  
 F:2905-2940/Domain: LDL receptor ligand-binding repeat homology <LDLK>  
 F:2945-2981/Domain: EGF homology <EG11>  
 F:2987-3022/Domain: EGF homology <EG12>  
 F:3030-3069/Domain: LDL receptor YWTD-containing repeat homology <YW34>  
 F:3070-3114/Domain: LDL receptor YWTD-containing repeat homology <YW35>  
 F:3115-3157/Domain: LDL receptor YWTD-containing repeat homology <YW36>  
 F:3158-3201/Domain: LDL receptor YWTD-containing repeat homology <YW37>  
 F:3202-3242/Domain: LDL receptor YWTD-containing repeat homology <YW38>  
 F:3243-3285/Domain: LDL receptor YWTD-containing repeat homology <YW39>  
 F:3295-3331/Domain: EGF homology <EG13>  
 F:3335-3370/Domain: LDL receptor ligand-binding repeat homology <LDLM>  
 F:3375-3409/Domain: LDL receptor ligand-binding repeat homology <LDLN>  
 F:3414-3449/Domain: LDL receptor ligand-binding repeat homology <LDLO>  
 F:3454-3490/Domain: LDL receptor ligand-binding repeat homology <LDLP>  
 F:3495-3532/Domain: LDL receptor ligand-binding repeat homology <LDLQ>  
 F:3537-3571/Domain: LDL receptor ligand-binding repeat homology <LDLR>  
 F:3576-3610/Domain: LDL receptor ligand-binding repeat homology <LDLS>  
 F:3614-3648/Domain: LDL receptor ligand-binding repeat homology <LDLT>  
 F:3655-3691/Domain: LDL receptor ligand-binding repeat homology <LDLU>  
 F:3696-3732/Domain: LDL receptor ligand-binding repeat homology <LDLV>  
 F:3742-3777/Domain: LDL receptor ligand-binding repeat homology <EG14>  
 F:3786-3823/Domain: EGF homology <EG15>  
 F:3829-3861/Domain: EGF homology <EG16>  
 F:3869-3912/Domain: LDL receptor YWTD-containing repeat homology <YW40>  
 F:3913-3970/Domain: LDL receptor YWTD-containing repeat homology <YW41>  
 F:3945-4545/Domain: alpha-2-macroglobulin receptor 85K chain #status predicted <85K>  
 F:3945-4421/Domain: 85K chain extracellular #status predicted <EXT>  
 F:3971-4013/Domain: LDL receptor YWTD-containing repeat homology <YW42>  
 F:4014-4057/Domain: LDL receptor YWTD-containing repeat homology <YW43>  
 F:4058-4100/Domain: LDL receptor YWTD-containing repeat homology <YW44>  
 F:4101-4143/Domain: LDL receptor YWTD-containing repeat homology <YW45>  
 F:4152-4183/Domain: EGF homology <EG16>  
 F:4201-4232/Domain: EGF homology <EG17>  
 F:4237-4268/Domain: EGF homology <EG18>  
 F:4273-4304/Domain: EGF homology <EG19>  
 F:4309-4340/Domain: EGF homology <EG20>  
 F:4345-4375/Domain: EGF homology <EG21>  
 F:4378-4409/Domain: EGF homology <EG22>  
 F:4422-4445/Domain: transmembrane #status predicted <TM>  
 F:4446-4545/Domain: intracellular #status predicted <INT>  
 F:167,2999/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted  
 F:2959/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
 F:4076,4126,4279/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 31.1%; Score 51; DB 1; Length 4545;  
 Best Local Similarity 41.7%; Pred. No. 2.8e+02;  
 Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 3 EVVCDRLGKKVXKCNVDTTIGD 26  
bb 3659 EFQCNNTLCKPLAWKCDGEDDCG 3682

RESULT 15

A25161  
tray protein - Salmonella typhimurium plasmid pSD208  
C;Species: Salmonella typhimurium  
C;Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 16-Feb-1997  
C;Accession: A25161  
R;Finlay, B.B.; Frost, L.S.; Paranchych, W.  
J;Bacteriol 168, 990-998, 1986  
A;Title: Nucleotide sequence of the trvA<sub>LS</sub> region from IncFV plasmid pSD208.  
A;Reference number: A91828; MUID:87056998; PMID:2877970  
A;Molecule type: DNA  
A;Residues: 1-69 <FIN>  
A;Cross-references: UNIPARC:UPI00001376DP  
C;Genetics:  
A;Gene: tray  
A;Genome: plasmid  
C;Keywords: DNA binding

Query Match 30.5%; Score 50; DB 2; Length 69;  
Best Local Similarity 44.4%; Pred. No. 10;  
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 10 LGKKVXKCNVDTTIGDL 27  
bb 10 IGKKVNISCLDAIDEL 27

Search completed: March 29, 2006, 09:07:57  
Job time : 41 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 29, 2006, 09:07:30 ; Search time 46 Seconds  
(without alignments)  
59.311 Million cell updates/sec

Title: US-10-067-832D-14  
Perfect score: 164  
Sequence: 1 MIEVVCNDRLGKKVXVKCNTDTIGDLKKLIAA 33

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/prodata/1/iaa/6\_COMB.pep.\*  
3: /cgn2\_6/prodata/1/iaa/H\_COMB.pep.\*  
4: /cgn2\_6/prodata/1/iaa/PCTUS\_COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/R8\_COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfilese1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	163	99.4	33	2	US-09-331-930A-14
2	163	99.4	73	2	US-09-331-930A-2
3	163	99.4	73	2	US-09-331-930A-19
4	163	99.4	73	2	US-09-331-930A-20
5	163	99.4	73	2	US-09-331-930A-21
6	163	99.4	73	2	US-09-331-930A-24
7	163	99.4	73	2	US-09-331-930A-25
8	135	82.3	73	2	US-09-331-930A-22
9	106	64.6	66	2	US-09-331-930A-23
10	106	64.6	75	2	US-09-248-796A-16302
11	52	31.7	231	2	US-09-107-532A-5301
12	52	31.7	1094	2	US-09-268-347-32
13	51	31.1	4544	1	US-08-469-486-52
14	51	31.1	4544	1	US-08-469-658-52
15	50	30.5	482	2	US-09-270-767-43292
16	49	29.9	113	2	US-09-173-300-54
17	49	29.9	113	2	US-10-027-450-54
18	49	29.9	347	2	US-09-270-767-57323
19	49	29.9	348	2	US-09-248-796A-18141
20	49	29.9	349	2	US-09-270-767-42065
21	48	29.3	359	2	US-09-516-143A-4
22	48	29.3	359	2	US-09-984-205-4
23	48	29.3	359	2	US-10-759-277-4
24	48	29.3	359	2	US-09-930-440C-6
25	48	29.3	367	2	US-09-949-016-9749
26	48	29.3	1070	2	US-09-107-532A-6735
27	47.5	29.0	883	2	US-09-248-796A-20980

28	47	28.7	193	2	US-08-671-548C-16
29	47	28.7	193	2	US-08-284-667A-16
30	47	28.7	262	2	US-09-328-352-5050
31	46	28.0	455	2	US-09-221-235-5
32	46	28.0	455	2	US-09-221-928-5
33	46	28.0	455	2	US-09-221-527-5
34	46	28.0	455	2	US-09-221-236-5
35	46	28.0	455	2	US-09-221-416-5
36	46	28.0	455	2	US-09-221-245-5
37	46	28.0	455	2	US-09-163-115-5
38	46	28.0	455	2	US-09-221-528-5
39	46	28.0	455	2	US-09-593-553-5
40	46	28.0	455	2	US-09-221-237-5
41	46	28.0	455	2	US-09-399-588-2
42	46	28.0	455	2	US-09-757-982-5
43	46	28.0	532	1	US-08-481-337A-6
44	46	28.0	532	2	US-09-382-256-6
45	46	28.0	532	2	US-09-382-256-14

ALIGNMENTS

RESULT 1  
US-09-331-930A-14  
; Sequence 14, Application US/09331930A  
; Patent No. 6436670  
; GENERAL INFORMATION:  
; APPLICANT: ZIMMET, PAUL Z.  
; APPLICANT: COLLIER, GREGORY  
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR  
; FILE REFERENCE: 22975-20007.00  
; CURRENT APPLICATION NUMBER: US/09/331,930A  
; CURRENT FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: PCT/AU98/00902  
; PRIOR FILING DATE: 1998-10-30  
; PRIOR APPLICATION NUMBER: AU P0117/97  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: AU P0323/97  
; PRIOR FILING DATE: 1997-11-11  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (15)  
; OTHER INFORMATION: variable amino acid  
US-09-331-930A-14  
  
Query Match 99.4%; Score 163; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 5.2e-16; Indels 0; Gaps 0;  
Matches 33; Conservative 0; Mismatches 0;  
  
QY 1 MIEVVCNDRLGKKVXVKCNTDTIGDLKKLIAA 33  
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DB 1 MIEVVCNDRLGKKVXVKCNTDTIGDLKKLIAA 33  
  
RESULT 2  
US-09-331-930A-2  
; Sequence 2, Application US/09331930A  
; Patent No. 6436670  
; GENERAL INFORMATION:  
; APPLICANT: ZIMMET, PAUL Z.  
; APPLICANT: COLLIER, GREGORY  
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR  
; FILE REFERENCE: 22975-20007.00  
; CURRENT APPLICATION NUMBER: US/09/331,930A  
; CURRENT FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: PCT/AU98/00902

; PRIOR FILING DATE: 1998-10-30  
; PRIOR APPLICATION NUMBER: AU PP0117/97  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: AU PP0323/97  
; PRIOR FILING DATE: 1997-11-11  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 73  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Amino acid  
; OTHER INFORMATION: sequence for beacon from unknown organism  
US-09-331-930A-2

Query Match 99.4%; Score 163; DB 2; Length 73;  
Best Local Similarity 97.0%; Pred. No. 1.2e-15;  
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKKVVKCNTDDTTIGDLKKLIAA 33  
|||||  
DB 1 MIEVVCNDRLGKKVVKCNTDDTTIGDLKKLIAA 33

## RESULT 3

US-09-331-930A-19  
; Sequence 19, Application US/09331930A  
; Patent No. 6436670  
; GENERAL INFORMATION:  
; APPLICANT: ZIMMET, PAUL Z.  
; APPLICANT: COLLIER, GREGORY  
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR  
; FILE REFERENCE: 22975-20007.00  
; CURRENT APPLICATION NUMBER: US/09/331,930A  
; CURRENT FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: PCT/AU98/00902  
; PRIOR FILING DATE: 1998-10-30  
; PRIOR APPLICATION NUMBER: AU PP0117/97  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: AU PP0323/97  
; PRIOR FILING DATE: 1997-11-11  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 73  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Amino acid  
; OTHER INFORMATION: sequence for beacon from unknown organism  
US-09-331-930A-19

Query Match 99.4%; Score 163; DB 2; Length 73;  
Best Local Similarity 97.0%; Pred. No. 1.2e-15;  
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKKVVKCNTDDTTIGDLKKLIAA 33  
|||||  
DB 1 MIEVVCNDRLGKKVVKCNTDDTTIGDLKKLIAA 33

## RESULT 4

US-09-331-930A-20  
; Sequence 20, Application US/09331930A  
; Patent No. 6436670  
; GENERAL INFORMATION:  
; APPLICANT: ZIMMET, PAUL Z.  
; APPLICANT: COLLIER, GREGORY  
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR  
; FILE REFERENCE: 22975-20007.00  
; CURRENT APPLICATION NUMBER: US/09/331,930A  
; CURRENT FILING DATE: 1999-06-30

; PRIOR APPLICATION NUMBER: PCT/AU98/00902  
; PRIOR FILING DATE: 1998-10-30  
; PRIOR APPLICATION NUMBER: AU PP0117/97  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: AU PP0323/97  
; PRIOR FILING DATE: 1997-11-11  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 73  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-331-930A-20

Query Match 99.4%; Score 163; DB 2; Length 73;  
Best Local Similarity 97.0%; Pred. No. 1.2e-15;  
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKKVVKCNTDDTTIGDLKKLIAA 33  
|||||  
DB 1 MIEVVCNDRLGKKVVKCNTDDTTIGDLKKLIAA 33

## RESULT 5

US-09-331-930A-21  
; Sequence 21, Application US/09331930A  
; Patent No. 6436670  
; GENERAL INFORMATION:  
; APPLICANT: ZIMMET, PAUL Z.  
; APPLICANT: COLLIER, GREGORY  
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR  
; FILE REFERENCE: 22975-20007.00  
; CURRENT APPLICATION NUMBER: US/09/331,930A  
; CURRENT FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: PCT/AU98/00902  
; PRIOR FILING DATE: 1998-10-30  
; PRIOR APPLICATION NUMBER: AU PP0117/97  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: AU PP0323/97  
; PRIOR FILING DATE: 1997-11-11  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 73  
; TYPE: PRT  
; ORGANISM: Murine sp.  
US-09-331-930A-21

Query Match 99.4%; Score 163; DB 2; Length 73;  
Best Local Similarity 97.0%; Pred. No. 1.2e-15;  
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKKVVKCNTDDTTIGDLKKLIAA 33  
|||||  
DB 1 MIEVVCNDRLGKKVVKCNTDDTTIGDLKKLIAA 33

## RESULT 6

US-09-331-930A-24  
; Sequence 24, Application US/09331930A  
; Patent No. 6436670  
; GENERAL INFORMATION:  
; APPLICANT: ZIMMET, PAUL Z.  
; APPLICANT: COLLIER, GREGORY  
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR  
; FILE REFERENCE: 22975-20007.00  
; CURRENT APPLICATION NUMBER: US/09/331,930A  
; CURRENT FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: PCT/AU98/00902  
; PRIOR FILING DATE: 1998-10-30  
; PRIOR APPLICATION NUMBER: AU PP0117/97  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: AU PP0323/97

; PRIOR FILING DATE: 1997-11-11  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 73  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-09-331-930A-24

Query Match 99.4%; Score 163; DB 2; Length 73;  
Best Local Similarity 97.0%; Pred. No. 1.2e-15;  
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVNCNDRLGKVKVKNCTDDTIGDLKKLIAA 33  
DB 1 MIEVNCNDRLGKVKVKNCTDDTIGDLKKLIAA 33

## RESULT 7

US-09-331-930A-25  
; Sequence 25, Application US/09331930A  
; Patent No. 6436670  
; GENERAL INFORMATION:  
; APPLICANT: ZIMMET, PAUL Z.  
; APPLICANT: COLLIER, GREGORY  
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR  
; FILE REFERENCE: 22975-20007.00  
; CURRENT APPLICATION NUMBER: US/09/331,930A  
; CURRENT FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: PCT/AU98/00902  
; PRIOR FILING DATE: 1998-10-30  
; PRIOR APPLICATION NUMBER: AU PP0117/97  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: AU PP0323/97  
; PRIOR FILING DATE: 1997-11-11  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 25  
; LENGTH: 73  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-09-331-930A-25

Query Match 99.4%; Score 163; DB 2; Length 73;  
Best Local Similarity 97.0%; Pred. No. 1.2e-15;  
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVNCNDRLGKVKVKNCTDDTIGDLKKLIAA 33  
DB 1 MIEVNCNDRLGKVKVKNCTDDTIGDLKKLIAA 33

## RESULT 8

US-09-331-930A-22  
; Sequence 22, Application US/09331930A  
; Patent No. 6436670  
; GENERAL INFORMATION:  
; APPLICANT: ZIMMET, PAUL Z.  
; APPLICANT: COLLIER, GREGORY  
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR  
; FILE REFERENCE: 22975-20007.00  
; CURRENT APPLICATION NUMBER: US/09/331,930A  
; CURRENT FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: PCT/AU98/00902  
; PRIOR FILING DATE: 1998-10-30  
; PRIOR APPLICATION NUMBER: AU PP0117/97  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: AU PP0323/97  
; PRIOR FILING DATE: 1997-11-11  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 73

; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-09-331-930A-22

Query Match 82.3%; Score 135; DB 2; Length 73;  
Best Local Similarity 78.8%; Pred. No. 9.6e-12;  
Matches 26; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MIEVNCNDRLGKVKVKNCTDDTIGDLKKLIAA 33  
DB 1 MIEITVNDRLGKVKVKNCTDDTIGDLKKLIAA 33

## RESULT 9

US-09-331-930A-23  
; Sequence 23, Application US/09331930A  
; Patent No. 6436670  
; GENERAL INFORMATION:  
; APPLICANT: ZIMMET, PAUL Z.  
; APPLICANT: COLLIER, GREGORY  
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR  
; FILE REFERENCE: 22975-20007.00  
; CURRENT APPLICATION NUMBER: US/09/331,930A  
; CURRENT FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: PCT/AU98/00902  
; PRIOR FILING DATE: 1998-10-30  
; PRIOR APPLICATION NUMBER: AU PP0117/97  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: AU PP0323/97  
; PRIOR FILING DATE: 1997-11-11  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 66  
; TYPE: PRT  
; ORGANISM: Fasciola hepatica  
US-09-331-930A-23

Query Match 64.6%; Score 106; DB 2; Length 66;  
Best Local Similarity 80.8%; Pred. No. 9.8e-08;  
Matches 21; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 8 DRLGKVKVKNCTDDTIGDLKKLIAA 33  
DB 1 DRLGKVKVKNCTDDTIGDLKKLIAA 26

## RESULT 10

US-09-248-796A-16302  
; Sequence 16302, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 16302  
; LENGTH: 75  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-16302

Query Match 64.6%; Score 106; DB 2; Length 75;  
Best Local Similarity 61.3%; Pred. No. 1.1e-07;  
Matches 19; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy	1	MIEVVCNDRIGKVKVVKCNTDDTIGDLKLI	31
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Db	3	MIEIQANDRIGKKIKLKCLETDTIGDVKKIL	33

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RESULT 12

US-09-368-347-32

Sequence 32, Application US/09268347

Patent No. 6335182

GENERAL INFORMATION:

APPLICANT: Loosmore, Sheena M.

TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS

FILE REFERENCE: 1038-860

```

; CURRENT APPLICATION NUMBER: US/09/268,347
; CURRENT FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 1094
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-268-347-32

Query Match      31.7%; Score 52; DB 2; Length 1094;
Best Local Similarity 57.9%; Pred. No. 62;
Matches 11; Conservative 3; Mismatches 5; Indels

Qy      12 KQVXVKCNDTDTGDLKKL 30
      ||:| || ||:|:|:|
Db      100 KCLLVDDNTAATVGDRLKL 118

RESULT 13
US-08-469-486-52
; Sequence 52, Application US/08469486
; Patent No. 5739281
; GENERAL INFORMATION:
; APPLICANT: Thoegeersen, Hans Christian
; APPLICANT: Holtet, Thor Las
; APPLICANT: Etzerodt, Michael
; TITLE OF INVENTION: Improved method for the refolding of
; TITLE OF INVENTION: proteins
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; SOFTWARE: #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,486
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/192,060
; FILING DATE: February 4, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06363/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 542 5070
; TELEFAX: 617 542 8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4544 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-469-486-52

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Db 3658 EFQCNNTLCKPLAWKCDGEDDCGD 3681

RESULT 14

US-08-469-658-52  
; Sequence 52, Application US/08469658  
; Patent No. 5917018  
; GENERAL INFORMATION:  
; APPLICANT: Th egersen, Hans Christian  
; APPLICANT: Holtet, Thor Las  
; APPLICANT: Eterodt, Michael  
; TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOLDING OF  
; TITLE OF INVENTION: PROTEINS  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version  
; SOFTWARE: #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/469,658  
; FILING DATE: June 5, 1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/192,060  
; FILING DATE: February 4, 1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Paul T. Clark  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 06363/002002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617 542 5070  
; TELEFAX: 617 542 8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 52:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4544 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-469-658-52

Query Match 31.1%; Score 51; DB 1; Length 4544;  
Best Local Similarity 41.7%; Pred. No. 3.7e+02;  
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 3 EVVQNDRLGKVKVKNCTDDTIGD 26

Db 3658 EFQCNNTLCKPLAWKCDGEDDCGD 3681

RESULT 15

US-09-270-767-43292  
; Sequence 43292, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 43292  
; LENGTH: 482  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
; FEATURE:  
; OTHER INFORMATION: Xaa means any amino acid  
US-09-270-767-43292

Query Match 30.5%; Score 50; DB 2; Length 482;  
Best Local Similarity 57.9%; Pred. No. 51;  
Matches 11; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 13 KVVVKCNTDDTIGDLKKLI 31

Db 406 KTFVKCNKKEQKDLKKLI 424

Search completed: March 29, 2006, 09:08:49  
Job time : 47 secs

**THIS PAGE BLANK (USP10)**

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2006, 09:08:10 ; Search time 165 Seconds  
(without alignments)  
83.566 Million cell updates/sec

Title: US-10-067-832D-14

Perfect score: 164

Sequence: 1 MIEVVCNDRLGKKVVKCNTDTTIGDLKKLIAA 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:\*

- 1: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 5: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /cgn2\_6/prodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	163	99.4	33	5	US-10-067-832D-14
2	163	99.4	68	4	US-10-424-599-250542
3	163	99.4	73	5	US-10-067-832D-2
4	163	99.4	73	5	US-10-067-832D-15
5	163	99.4	73	5	US-10-067-832D-16
6	163	99.4	73	5	US-10-067-832D-19
7	163	99.4	73	5	US-10-067-832D-20
8	163	99.4	73	5	US-10-965-898-68
9	163	99.4	115	4	US-10-264-049-2463
10	152	92.7	73	6	US-11-097-143-6522
11	146	89.0	73	4	US-10-424-599-212296
12	146	89.0	73	4	US-10-437-963-147593
13	146	89.0	73	4	US-10-767-701-46049
14	146	89.0	73	4	US-10-425-115-233843
15	146	89.0	73	4	US-10-425-115-233846
16	146	89.0	73	4	US-10-425-115-233848
17	146	89.0	73	4	US-10-425-115-233849
18	146	89.0	73	4	US-10-425-115-233851
19	146	89.0	73	4	US-10-425-115-233853
20	146	89.0	73	4	US-10-425-115-288480
21	146	89.0	73	4	US-10-425-115-288482
22	146	89.0	73	4	US-10-425-115-288483
23	146	89.0	73	4	US-10-425-115-288486
24	146	89.0	73	4	US-10-425-115-288481
25	137	83.5	73	4	US-10-425-115-288479
26	135	82.3	73	4	US-10-067-832D-17
27	134	81.7	89	4	US-10-425-115-355452

28	131.5	80.2	74	4	US-10-424-599-207467
29	130.5	79.6	73	5	US-10-739-930-8461
30	120	73.2	45	4	US-10-425-115-282612
31	118	72.0	71	4	US-10-424-599-147197
32	114	69.5	89	4	US-10-083-357-770
33	114	69.5	320	4	US-10-338-411-11
34	114	69.5	320	4	US-10-389-640-11
35	111	67.7	82	4	US-10-424-599-191611
36	110	67.1	73	4	US-10-425-115-239033
37	106	64.6	66	5	US-10-067-832D-18
38	97	59.1	55	4	US-10-425-115-270723
39	97	59.1	110	4	US-10-424-599-213543
40	93	56.7	83	4	US-10-437-963-135926
41	84	51.2	59	4	US-10-425-115-356308
42	84	51.2	79	4	US-10-425-115-289824
43	68	41.5	27	3	US-09-864-761-41766
44	63	38.4	63	4	US-10-425-115-201973
45	60	36.6	64	4	US-10-424-599-271299

ALIGNMENTS

RESULT 1

US-10-067-832D-14  
; Sequence 14, Application US/10067832D  
; Publication No. US20050059108A1  
; GENERAL INFORMATION:  
; APPLICANT: ZIMMET, PAUL ZEV  
; APPLICANT: COLLIER, GREGORY  
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR  
; FILE REFERENCE: 229752000701  
; CURRENT APPLICATION NUMBER: US/10/067,832D  
; CURRENT FILING DATE: 2002-06-03  
; PRIOR APPLICATION NUMBER: 09/331,930  
; PRIOR FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: PCT/AU98/00902  
; PRIOR FILING DATE: 1998-10-30  
; PRIOR APPLICATION NUMBER: AU PP 0117  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: AU PP 0323  
; PRIOR FILING DATE: 1997-11-11  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: Patentin Ver. 3.2  
; SEQ ID NO 14  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (15)  
; OTHER INFORMATION: Leu, Pro, His, or Arg  
US-10-067-832D-14

Query Match 99.4%; Score 163; DB 5; Length 33;  
Best Local Similarity 100.0%; Pred. No. 2.1e-15;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKKVVKCNTDTTIGDLKKLIAA 33  
Db 1 MIEVVCNDRLGKKVVKCNTDTTIGDLKKLIAA 33

RESULT 2

US-10-424-599-250542  
; Sequence 250542, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(5323)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 250542  
; LENGTH: 68  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_6826C.1.pcp  
US-10-424-599-250542

Query Match 99.4%; Score 163; DB 4; Length 68;  
Best Local Similarity 97.0%; Pred. No. 4.5e-15;  
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVVKCNTDDTIGDLKGLIAA 33  
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DB 1 MIEVVCNDRLGKVKVVKCNTDDTIGDLKGLIAA 33

RESULT 3  
US-10-067-832D-2  
; Sequence 2, Application US/10067832D  
; Publication No. US20050059108A1  
; GENERAL INFORMATION:  
; APPLICANT: ZIMMET, PAUL ZEV  
; APPLICANT: COLLIER, GREGORY  
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR  
; FILE REFERENCE: 229752000701  
; CURRENT APPLICATION NUMBER: US/10/067,832D  
; CURRENT FILING DATE: 2002-06-03  
; PRIOR APPLICATION NUMBER: 09/331,930  
; PRIOR FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: PCT/AU98/00902  
; PRIOR FILING DATE: 1998-10-30  
; PRIOR APPLICATION NUMBER: AU PP 0117  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: AU PP 0323  
; PRIOR FILING DATE: 1997-11-11  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 2  
; LENGTH: 73  
; TYPE: PRT  
; ORGANISM: Psammomyes oboeaus  
US-10-067-832D-2

Query Match 99.4%; Score 163; DB 5; Length 73;  
Best Local Similarity 97.0%; Pred. No. 4.9e-15;  
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVVKCNTDDTIGDLKGLIAA 33  
|||||  
DB 1 MIEVVCNDRLGKVKVVKCNTDDTIGDLKGLIAA 33

RESULT 4  
US-10-067-832D-15  
; Sequence 15, Application US/10067832D  
; Publication No. US20050059108A1  
; GENERAL INFORMATION:  
; APPLICANT: ZIMMET, PAUL ZEV  
; APPLICANT: COLLIER, GREGORY  
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR  
; FILE REFERENCE: 229752000701  
; CURRENT APPLICATION NUMBER: US/10/067,832D  
; CURRENT FILING DATE: 2002-06-03  
; PRIOR APPLICATION NUMBER: 09/331,930  
; PRIOR FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: PCT/AU98/00902  
; PRIOR FILING DATE: 1998-10-30

; PRIOR APPLICATION NUMBER: AU PP 0117  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: AU PP 0323  
; PRIOR FILING DATE: 1997-11-11  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 15  
; LENGTH: 73  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-067-832D-15

Query Match 99.4%; Score 163; DB 5; Length 73;  
Best Local Similarity 97.0%; Pred. No. 4.9e-15;  
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVVKCNTDDTIGDLKGLIAA 33  
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DB 1 MIEVVCNDRLGKVKVVKCNTDDTIGDLKGLIAA 33

RESULT 5  
US-10-067-832D-16  
; Sequence 16, Application US/10067832D  
; Publication No. US20050059108A1  
; GENERAL INFORMATION:  
; APPLICANT: ZIMMET, PAUL ZEV  
; APPLICANT: COLLIER, GREGORY  
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR  
; FILE REFERENCE: 229752000701  
; CURRENT APPLICATION NUMBER: US/10/067,832D  
; CURRENT FILING DATE: 2002-06-03  
; PRIOR APPLICATION NUMBER: 09/331,930  
; PRIOR FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: PCT/AU98/00902  
; PRIOR FILING DATE: 1998-10-30  
; PRIOR APPLICATION NUMBER: AU PP 0117  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: AU PP 0323  
; PRIOR FILING DATE: 1997-11-11  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 16  
; LENGTH: 73  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-067-832D-16

Query Match 99.4%; Score 163; DB 5; Length 73;  
Best Local Similarity 97.0%; Pred. No. 4.9e-15;  
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVVKCNTDDTIGDLKGLIAA 33  
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DB 1 MIEVVCNDRLGKVKVVKCNTDDTIGDLKGLIAA 33

RESULT 6  
US-10-067-832D-19  
; Sequence 19, Application US/10067832D  
; Publication No. US20050059108A1  
; GENERAL INFORMATION:  
; APPLICANT: ZIMMET, PAUL ZEV  
; APPLICANT: COLLIER, GREGORY  
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR  
; FILE REFERENCE: 229752000701  
; CURRENT APPLICATION NUMBER: US/10/067,832D  
; CURRENT FILING DATE: 2002-06-03  
; PRIOR APPLICATION NUMBER: 09/331,930  
; PRIOR FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: PCT/AU98/00902  
; PRIOR FILING DATE: 1998-10-30  
; PRIOR APPLICATION NUMBER: AU PP 0117



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; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP 0323
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 19
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-067-832D-19

Query Match          99.4%; Score 163; DB 5; Length 73;
Best Local Similarity 97.0%; Pred. No. 4.9e-15;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKKVVKCNTDDTTIGDLKKLIAA 33
Db 1 MIEVVCNDRLGKKVVKCNTDDTTIGDLKKLIAA 33

RESULT 7
US-10-067-832D-20
; Sequence 20, Application US/10067832D
; Publication No. US20050059108A1
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL ZEV
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975200701
; CURRENT APPLICATION NUMBER: US/10/067,832D
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 09/331,930
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP 0117
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP 0323
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 20
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-067-832D-20

Query Match          99.4%; Score 163; DB 5; Length 73;
Best Local Similarity 97.0%; Pred. No. 4.9e-15;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKKVVKCNTDDTTIGDLKKLIAA 33
Db 1 MIEVVCNDRLGKKVVKCNTDDTTIGDLKKLIAA 33

RESULT 8
US-10-965-898-68
; Sequence 68, Application US/10965898
; Publication No. US20050084936A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: HUMAN REGULATORY PROTEINS
; NUMBER OF SEQUENCES: 150
; CORRESPONDENCE ADDRESS:
; Bandman, Olga
; Hillman, Jennifer L.
; Au-Young, Janice
; Tang, Y. Tom
; Yue, Henry
; Shah, Purvi
; Guegler, Karl J.
; Corley, Neil C.
; TITLE OF INVENTION: HUMAN REGULATORY PROTEINS
; NUMBER OF SEQUENCES: 150
; CORRESPONDENCE ADDRESS:

; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP 0323
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 19
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-067-832D-19

Query Match          99.4%; Score 163; DB 5; Length 73;
Best Local Similarity 97.0%; Pred. No. 4.9e-15;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKKVVKCNTDDTTIGDLKKLIAA 33
Db 1 MIEVVCNDRLGKKVVKCNTDDTTIGDLKKLIAA 33

RESULT 9
US-10-264-049-2463
; Sequence 2463, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P4133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2463
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-2463

Query Match          99.4%; Score 163; DB 4; Length 115;
Best Local Similarity 97.0%; Pred. No. 8e-15;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKKVVKCNTDDTTIGDLKKLIAA 33
Db 1 MIEVVCNDRLGKKVVKCNTDDTTIGDLKKLIAA 33
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Db 43 MIEVVCNDRLGKVKVCKNTDGTGDLKGLIAA 75  
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RESULT 10  
US-11-097-143-6522  
; Sequence 6522, Application US/11097143  
; Publication No. US20050208558A1  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig  
; APPLICANT: et al.  
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
; TITLE OF INVENTION: CL000728  
; FILE REFERENCE: CL000728  
; CURRENT APPLICATION NUMBER: US/11/097,143  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: 60/157,832  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: 60/160,191  
; PRIOR FILING DATE: 1999-10-19  
; PRIOR APPLICATION NUMBER: 60/161,932  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: 60/164,769  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/173,383  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: 60/175,693  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/184,831  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/191,637  
; PRIOR FILING DATE: 2000-03-23  
; NUMBER OF SEQ ID NOS: 43008  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6522  
; LENGTH: 73  
; TYPE: PRT  
; ORGANISM: DROSOPHILA  
US-11-097-143-6522

Query Match 92.7%; Score 152; DB 6; Length 73;  
Best Local Similarity 87.9%; Pred. No. 1.7e-13;  
Matches 29; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVCKNTDGTGDLKGLIAA 33  
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Db 1 MIEITCNDRLGKVKVCKNPDGTGDLKGLIAA 33  
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RESULT 11  
US-10-424-599-212296  
; Sequence 212296, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J  
; APPLICANT: Kovalic, David K  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 212296  
; LENGTH: 73  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_33729C.1.pep  
US-10-424-599-212296

Query Match 89.0%; Score 146; DB 4; Length 73;  
Best Local Similarity 87.9%; Pred. No. 1.1e-12;  
Matches 29; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVCKNTDGTGDLKGLIAA 33  
|||||

Db 1 MIEVVLNDRLGKVKVCKNDDTTGDLKGLVAA 33  
|||||

RESULT 12  
US-10-437-963-147593  
; Sequence 147593, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 147593  
; LENGTH: 73  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_48107C.1.pep  
US-10-437-963-147593

Query Match 89.0%; Score 146; DB 4; Length 73;  
Best Local Similarity 87.9%; Pred. No. 1.1e-12;  
Matches 29; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVCKNTDGTGDLKGLIAA 33  
|||||

Db 1 MIEVVLNDRLGKVKVCKNDDTTGDLKGLVAA 33  
|||||

RESULT 13  
US-10-767-701-46049  
; Sequence 46049, Application US/10767701  
; Publication No. US20040172684A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement  
; FILE REFERENCE: 38-21(53353)B  
; CURRENT APPLICATION NUMBER: US/10/767,701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 46049  
; LENGTH: 73  
; TYPE: PRT  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C594\_1.pep  
US-10-767-701-46049

Query Match 89.0%; Score 146; DB 4; Length 73;  
Best Local Similarity 87.9%; Pred. No. 1.1e-12;  
Matches 29; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVCKNTDGTGDLKGLIAA 33  
|||||

```
Db      1 MIEVVLNDRLGKKVVKCNEDDTIGDLKKLVAA 33
>
RESULT 14
US-10-425-115-233843
; Sequence 233843, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 233843
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_144858C.1.pap
US-10-425-115-233843

Query Match      89.0%; Score 146; DB 4; Length 73;
Best Local Similarity 87.9%; Pred. No. 1.1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 MIEVVCNDRLGKKVVKCNEDDTIGDLKKLVAA 33
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MIEVVLNDRLGKKVVKCNEDDTIGDLKKLVAA 33

RESULT 15
US-10-425-115-233846
; Sequence 233846, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 233846
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_144860C.1.pap
US-10-425-115-233846

Query Match      89.0%; Score 146; DB 4; Length 73;
Best Local Similarity 87.9%; Pred. No. 1.1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 MIEVVCNDRLGKKVVKCNEDDTIGDLKKLVAA 33
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MIEVVLNDRLGKKVVKCNEDDTIGDLKKLVAA 33

Search completed: March 29, 2006, 09:11:39
Job time : 165 secs
```

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## **Protein Sequence Searches - February 2005**

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rwp**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

---

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Matches 14; Conservative 4; Mismatches 6; Indels

Best local similarity	50.00	12.00	11.7
Matches	14: Conservative	4: Mismatches	6: Indels
			14: Gaps

```
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 17311
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; NAME/KEY: misc_feature
; LOCATION: (1)..(375)
; OTHER INFORMATION: Ceres Seq. ID no. 12357280
US-11-096-568A-17311

Query Match      30.5%; Score 50; DB 7; Length 375;
Best Local Similarity 40.0%; Pred. No. 6;
Matches 12; Conservative 7; Mismatches 7; Indels 4; Gaps 1;

QY      2 IEVVCNDRLGKKVKVKCNCTDDTIGDLKKLI 31
Db      154 IDLYOHRIDKKVPFIEV---TIGELKKLV 179

RESULT 8
US-11-004-399-3161
; Sequence 3161, Application US/11004399
; Publication No. US20060053516A1
; GENERAL INFORMATION:
; APPLICANT: Chye, Mee Lee
; APPLICANT: Li, Hong Ye
; APPLICANT: Ramalingam, Sathiekumar
; APPLICANT: Foon, Leo Lit Man
; TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide
; TITLE OF INVENTION: Sequences and Methods of Use Thereof For Immunization Against SA
; FILE REFERENCE: 2587/73166/RDK
; CURRENT APPLICATION NUMBER: US/11/004,399
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,637
; PRIOR FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 4043
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3161
; LENGTH: 47
; TYPE: PRT
; ORGANISM: SARS-CoV Virus
US-11-004-399-3161

Query Match      29.3%; Score 48; DB 7; Length 47;
Best Local Similarity 50.0%; Pred. No. 1.1;
Matches 7; Conservative 4; Mismatches 3; Indels 3; Gaps 0;

QY      16 VKCNTDDTIGDLKK 29
Db      23 IDCNTDETSSLOK 36

RESULT 9
US-11-123-013-6
; Sequence 6, Application US/11123013
; Publication No. US20050287637A1
; GENERAL INFORMATION:
; APPLICANT: Betenbaugh, Michael J.
; APPLICANT: Lawrence, Shawn J.
; APPLICANT: Lee, Yuan C.
; APPLICANT: Coleman, Timothy A.
; TITLE OF INVENTION: Engineering Intracellular Sialylation Pathways
; FILE REFERENCE: 03940077bp
; CURRENT APPLICATION NUMBER: US/11/123,013
; CURRENT FILING DATE: 2005-05-06
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; PRIOR APPLICATION NUMBER: US 60/122,582
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: US 60/169,624
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 60/227,579
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 09/516,793
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 09/930,440
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-123-013-6

Query Match      29.3%; Score 48; DB 7; Length 359;
Best Local Similarity 53.3%; Pred. No. 11;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      3 EVVCNDRLGKKVKVK 17
Db      284 EMACNEKLGKSVYAK 298

RESULT 10
US-11-096-568A-31955
; Sequence 31955, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 31955
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: misc_feature
; LOCATION: (1)..(114)
; OTHER INFORMATION: Ceres Seq. ID no. 13591797
US-11-096-568A-31955

Query Match      28.7%; Score 47; DB 7; Length 114;
Best Local Similarity 36.8%; Pred. No. 4.4;
Matches 14; Conservative 4; Mismatches 6; Indels 14; Gaps 3;

QY      1 MIEVVCNDRLGKKVKV-----KC-----NTDDTIG 25
Db      78 MVQILCND-CGKAEVQVHVVAQKCPNCKSYNTRQTRG 114

RESULT 11
US-11-096-568A-31954
; Sequence 31954, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 31954
; LENGTH: 175
; TYPE: PRT
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human LDL-receptor class A domain
US-10-957-351-107

Query Match      31.1%; Score 51; DB 6; Length 37;
Best Local Similarity 41.7%; Pred. No. 0.31;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 3 EVVQNDRLGKKVKKVKNCTDDTTIGD 26
Db 5 EFQCNNTLCKPLAWKCDGEDDCGD 28

RESULT 3
US-10-501-035-214
; Sequence 214, Application US/10501035
; Publication No. US20060046249A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
; TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASE
; FILE REFERENCE: D0185 PCT
; CURRENT APPLICATION NUMBER: US/10/501,035
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/350,061
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 795
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 214
; LENGTH: 4544
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-501-035-214

Query Match      31.1%; Score 51; DB 6; Length 4544;
Best Local Similarity 41.7%; Pred. No. 71;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 3 EVVQNDRLGKKVKKVKNCTDDTTIGD 26
Db 3658 EFQCNNTLCKPLAWKCDGEDDCGD 3681

RESULT 4
US-11-076-427A-32
; Sequence 32, Application US/11076427A
; Publication No. US20060025338A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, et al.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF LYMPHATIC AND VENO
; TITLE OF INVENTION: VESSEL ARTERIALIZATION
; FILE REFERENCE: 28967/40008A
; CURRENT APPLICATION NUMBER: US/11/076,427A
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US 60/551,581
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32
; LENGTH: 4544
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-076-427A-32

Query Match      31.1%; Score 51; DB 7; Length 4544;
Best Local Similarity 41.7%; Pred. No. 71;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
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```
QY 3 EVVQNDRLGKKVKKVKNCTDDTTIGD 26
Db 3658 EFQCNNTLCKPLAWKCDGEDDCGD 3681

RESULT 5
US-11-096-568A-17313
; Sequence 17313, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 17313
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(319)
; OTHER INFORMATION: Ceres Seq. ID no. 12357282
US-11-096-568A-17313

Query Match      30.5%; Score 50; DB 7; Length 319;
Best Local Similarity 40.0%; Pred. No. 5;
Matches 12; Conservative 7; Mismatches 7; Indels 4; Gaps 1;

QY 2 IEVQNDRLGKKVKKVKNCTDDTTIGDLKKLI 31
Db 98 IDLYYQHRIDKKVPIEV---TIGELKKLV 123

RESULT 6
US-11-096-568A-17312
; Sequence 17312, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 17312
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(346)
; OTHER INFORMATION: Ceres Seq. ID no. 12357281
US-11-096-568A-17312

Query Match      30.5%; Score 50; DB 7; Length 346;
Best Local Similarity 40.0%; Pred. No. 5.4;
Matches 12; Conservative 7; Mismatches 7; Indels 4; Gaps 1;

QY 2 IEVQNDRLGKKVKKVKNCTDDTTIGDLKKLI 31
Db 125 IDLYYQHRIDKKVPIEV---TIGELKKLV 150

RESULT 7
US-11-096-568A-17311
; Sequence 17311, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	56.5	34.5	258	7	US-11-058-924-6	Sequence 6, Appli
2	51	31.1	37	6	US-10-957-351-107	Sequence 107, App
3	51	31.1	4544	6	US-10-501-035-214	Sequence 214, App
4	51	31.1	4544	7	US-11-076-427A-32	Sequence 32, Appl
5	50	30.5	319	7	US-11-096-568A-17313	Sequence 17313, A
6	50	30.5	346	7	US-11-096-568A-17312	Sequence 17312, A
7	50	30.5	375	7	US-11-096-568A-17311	Sequence 17311, A
8	48	29.3	47	7	US-11-004-399-3161	Sequence 3161, Ap
9	48	29.3	359	7	US-11-123-013-6	Sequence 6, Appli
10	47	28.7	114	7	US-11-096-568A-31955	Sequence 31955, A
11	47	28.7	175	7	US-11-096-568A-31954	Sequence 31954, A
12	47	28.7	250	7	US-11-096-568A-30582	Sequence 30582, A
13	47	28.7	258	7	US-11-096-568A-30581	Sequence 30581, A
14	47	28.7	282	7	US-11-096-568A-30580	Sequence 30580, A
15	47	28.7	276	7	US-11-096-568A-31559	Sequence 31559, A
16	47	28.7	294	7	US-11-096-568A-31558	Sequence 31558, A
17	47	28.7	308	7	US-11-096-568A-31557	Sequence 31557, A
18	47	28.7	355	7	US-11-087-099-3395	Sequence 3295, Ap
19	47	28.7	584	7	US-11-096-568A-31265	Sequence 31265, A
20	47	28.7	610	7	US-11-096-568A-31264	Sequence 31264, A
21	47	28.7	640	7	US-11-096-568A-31263	Sequence 31263, A
22	46	28.0	247	7	US-11-096-568A-29306	Sequence 29306, A
23	46	28.0	256	7	US-11-096-568A-29305	Sequence 29305, A
24	46	28.0	311	7	US-11-096-568A-29304	Sequence 29304, A
25	46	28.0	314	7	US-11-096-568A-19764	Sequence 19764, A

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases: older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions **.rnpbm** (Published\_Applications\_NA\_Main) and **.rnpbn** (Published\_Applications\_NA\_New).

Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions **.rapbm** (Published\_Applications\_AA\_Main) and **.rapbn** (Published\_Applications\_AA\_New).

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GenCore version 5.1.1.7  
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OM protein - protein search, using sw model

Run on: March 29, 2006, 09:02:15 ; Search time 230 Seconds  
(without alignments)  
101.228 Million cell updates/sec

Title: US-10-067-832D-14  
Perfect score: 164  
Sequence: 1 MIEVVCNDRLGKKVXKNCNTDDTIGDLKLLIAA 33

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80.\*

1: uniprot\_prot.\*

2: uniprot\_treml.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	163	99.4	47	Q5BJS1_RAT	Q5bjs1 ratu
2	163	99.4	73	UBJ5_HUMAN	Q9b211 homo sapien
3	163	99.4	73	UBJ5_MESAU	Q9egx7 mesocricetu
4	163	99.4	73	UBJ5_MOUSE	Q9epv8 mus musculu
5	163	99.4	73	UBJ5_PSAOB	Q791b0 psammomya o
6	163	99.4	73	Q5RC10_PONPY	Q5rc10 pongo pygma
7	163	99.4	73	Q4R5J3_MACFA	Q4r5j3 macaca fasc
8	153	93.3	73	UBJ5_BRARE	Q78xf2 brachydanio
9	152	92.7	73	UBJ5_DROME	Q9v998 drosophila
10	151	92.1	73	Q5H2C1_XENLA	Q5h2c1 xenopus lae
11	150	91.5	73	Q7QHM2_ANOGA	Q7qhm2 anopheles g
12	147	89.6	73	Q4SM16_TETNG	Q4sm16 tetradodon n
13	146	89.0	73	UBJ5_ARATH	Q6k220 oryza sativ
14	146	89.0	73	Q6K220_ORYSA	Q6k220 oryza sativ
15	146	89.0	73	Q57QV8_ARATH	Q57qv8 arabidopsis
16	143	87.2	73	Q81545_PLAP7	Q81545 plasmodium
17	143	87.2	73	Q7RBM4_PLAYO	Q7rbw4 plasmodium
18	143	87.2	73	Q4YUJ7_PLABE	Q4yu77 plasmodium
19	142	86.6	73	Q9MIU1_ARATH	Q9miu1 arabidopsis
20	140	85.4	73	UBJ5_SCHPO	Q94650 schizosach
21	136	82.9	87	Q54Q03_DICDI	Q54q03 dictyosteli
22	135	82.3	73	UBJ5_CAEEL	P91302 caenorhabdi
23	135	82.3	73	Q617M9_CAEER	Q617m9 caenorhabdi
24	133	81.1	73	Q4F9W2_USTWA	Q4f9w2 uscilego ma
25	133	81.1	73	Q4WZ69_THRPA	Q4wz69 theileria p
26	133	81.1	76	Q4UBB9_THRAN	Q4ubeb theileria a
27	131	79.9	73	Q5BS57_SCHJA	Q5bs57 schistosoma
28	130	79.3	70	Q6CI04_YARLI	Q6ci04 yarrowia li
29	128	78.0	73	Q4VAF8_MOUSE	Q4vaf8 mus musculu
30	121	73.8	276	Q5KM54_CRYNE	Q5km54 cryptococcu
31	121	73.8	276	Q5K8L5_CRYNE	Q5k8l5 cryptococcu

32	120	73.2	73	1	HUB1_DEBHA	Q6bup7 debaromyce
33	117	71.3	73	1	HUB1_CANGA	Q6fix7 candida gla
34	116	70.7	74	1	HUB1_KLULA	Q6cu12 kluyveromyc
35	116	70.7	79	2	Q6CUI1_KLULA	Q6cu11 kluyveromyc
36	115	70.1	73	1	HUB1_ASHGO	Q756x3 ashbya gos
37	110	67.1	73	1	HUB1_YEAST	Q6q546 saccharomyc
38	96	58.5	79	2	Q5OP03_ENTHI	Q5op03 entamoeba h
39	86	52.4	616	2	Q5BCG2_EMENI	Q5bcg2 aspergillus
40	85	51.8	237	2	Q41016_GIBZE	Q41016 gibberella
41	69	42.1	239	2	Q52620_MAGGR	Q52620 magnaporthe
42	62	37.8	189	2	Q4WYK6_ASFFU	Q4wyk6 aspergillus
43	62	37.8	261	2	Q8X065_NEUCR	Q8x065 neurospora
44	57	34.8	166	2	Q4WMP9_ASFFU	Q4wmp9 aspergillus
45	56.5	34.5	282	1	NADA_AFLCA	P29241 aplysia cal

#### ALIGNMENTS

RESULT 1  
Q5BJS1\_RAT PRELIMINARY; PRT; 47 AA.  
AC Q5BJS1\_1  
DT 10-MAY-2005 (TREMBLrel. 30, Created)  
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)  
DE LOC500954 protein.  
GN Name=LOC500954;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP TISSUE=Brain;  
RC TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Brain;  
RG NIH MGC Project;  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC091358; AAH91358.1; -; mRNA.  
DR SMR; Q5BJS1; 1-47.  
SQ SEQUENCE 47 AA; 5400 MW; B8PE50E31B325338 CRC64;

Query Match 99.4%; Score 163; DB 2; Length 47;  
Best Local Similarity 97.0%; Pred. No. 2.9e-15;  
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKKVXKNCNTDDTIGDLKLLIAA 33

DB 1 MIEVVCNDRLGKKVXKNCNTDDTIGDLKLLIAA 33

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CC removed.
CC -----
DR EMBL; AF3131915; AAK14178.1; -; mRNA.
DR EMBL; BT007355; AAP36019.1; -; mRNA.
DR EMBL; BC007053; AAH07053.1; -; mRNA.
DR PDB; 1POR; NMR; AA=1-73.
DR Ensembl; ENSG00000198258; Homo sapiens.
DR HGNC; HGNC:13736; UBL5.
DR H-InvDB; HIX0014729; -.
DR MIM; 606849; -.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; ubiquitin; 1.
DR PROSITE; PS00299; UBIQUITIN_1; FALSE NEG.
DR PROSITE; PS0053; UBIQUITIN_2; FALSE NEG.
DR 3D-structure; Ubl conjugation pathway.
KW DOMAIN 1 73 Ubiquitin-like.
SQ SEQUENCE 73 AA; 8547 MW; D68BC941536AA39F CRC64;

Query Match 99.4%; Score 163; DB 1; Length 73;
Best Local Similarity 97.0%; Pred. No. 4.5e-15;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKGVKVCNTDQDTIGDLKLLIAA 33
DB 1 MIEVVCNDRLGKGVKVCNTDQDTIGDLKLLIAA 33

RESULT 3
UBL5_MESAU
ID UBL5_MESAU STANDARD; PRT; 73 AA.
AC Q6EGX7;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ubiquitin-like protein 5 (Beacon protein).
GN Name=UBL5;
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Cricetidae; Cricetinae; Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Revel F., Simonneau V., Sorensen B.H., Mikkelsen J.D.;
RL "Beacon in the golden hamster.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SUBUNIT: Interacts with CLK4 (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Contains 1 ubiquitin-like domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AY329082; AAQ99044.1; -; mRNA.
DR SMR; Q8EGX7; 1-73.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; ubiquitin; 1.
DR PROSITE; PS00299; UBIQUITIN_1; FALSE NEG.
DR PROSITE; PS0053; UBIQUITIN_2; FALSE NEG.
DR Ubl conjugation pathway.
KW DOMAIN 1 73 Ubiquitin-like.
FT SEQUENCE 73 AA; 8547 MW; D68BC941536AA39F CRC64;

Query Match 99.4%; Score 163; DB 1; Length 73;
Best Local Similarity 97.0%; Pred. No. 4.5e-15;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKGVKVCNTDQDTIGDLKLLIAA 33
DB 1 MIEVVCNDRLGKGVKVCNTDQDTIGDLKLLIAA 33

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Db 1 MIEVNCNDRLGKKVRVKVKNCTDDTIGDLKKLIAA 33
RESULT 4
ID UBL5 MOUSE STANDARD; PRT; 73 AA.
AC Q9EPV8;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DE Ubiquitin-like protein 5.
GN Name=UBL5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J; TISSUE=Kidney Pancreas, Spinal ganglion, and Tongue;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojohori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson J.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Nagashima T., Numata K., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita K.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
[2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.C., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahay J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."

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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -1- SUBUNIT: Interacts with CLK4 (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Contains 1 ubiquitin-like domain.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC removed.
CC
CC EMBL; AK002730; BAB22312.1; -; mRNA.
CC EMBL; AK003992; BAB23111.1; -; mRNA.
CC EMBL; AK007726; BAB25215.1; -; mRNA.
CC EMBL; AK009854; BAB26545.1; -; mRNA.
CC EMBL; AK012803; BAB28481.1; -; mRNA.
CC EMBL; AK051149; BAC34537.1; -; mRNA.
CC EMBL; BC028498; AAB28498.1; -; mRNA.
CC PDB; 1UH6; NMR; A=1-73.
CC MGI; MGI:1913427; Ubl5.
CC InterPro; IPR000626; Ubiquitin.
CC Pfam; PF00240; ubiquitin; 1.
CC PROSITE; PS00299; UBIQUITIN_1; FALSE NEG.
CC PROSITE; PS0053; UBIQUITIN_2; FALSE NEG.
CC 3D-structure; Ubl conjugation pathway.
KW DOMAIN 1 73 Ubiquitin-like.
FT SEQUENCE 73 AA; 8547 MW; D68BC94153GAA39F CRC64;
SQ
Query Match 99.4%; Score 163; DB 1; Length 73;
Best Local Similarity 97.0%; Pred. No. 4.5e-15;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MIEVNCNDRLGKKVRVKVKNCTDDTIGDLKKLIAA 33
DB 1 MIEVNCNDRLGKKVRVKVKNCTDDTIGDLKKLIAA 33
RESULT 5
UBL5 PSAOB STANDARD; PRT; 73 AA.
AC Q791B0;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ubiquitin-like protein 5 (Beacon protein).
GN Name=UBL5;
OS Psammomya obesus (Fat sea rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Gerbillinae; Psammomys.
OX NCBI_TaxID=48139;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Hypothalamus;
RX MEDLINE=20527879; PubMed=11078442;
RA Collier G.R., McMillan J.S., Windmill K., Walder K., Tenne-Brown J.,
RA de Silva A., Trevisan P.J., Jones S., Morton G.J., Lee S., Augert G.,
RA Civitarese A., Zimmatt P.Z.;
RA "Beacon: a novel gene involved in the regulation of energy balance.";
RL Diabetea 49:1766-1771 (2000).
CC -1- SUBUNIT: Interacts with CLK4 (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Contains 1 ubiquitin-like domain.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF318186; AAG34704.1; -; mRNA.
CC SMR; Q791B0; 1-73.
CC InterPro; IPR000626; Ubiquitin.

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DR Pfan; PF00240; ubiquitin; 1.
DR PROSITE; PS00299; UBIQUITIN_1; FALSE_NEG.
DR PROSITE; PS00053; UBIQUITIN_2; FALSE_NEG.
KW Ubl conjugation pathway.
SQ DOMAIN 1 73 Ubiquitin-like.
FT SEQUENCE 73 AA; 8547 MW; D68BC941536AA39F CRC64;

Query Match          99.4%; Score 163; DB 1; Length 73;
Best Local Similarity 97.0%; Pred. No. 4.5e-15;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAA 33
Db 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAA 33

RESULT 6
QSRCIO_PONPY
ID QSRCIO_PONPY PRELIMINARY; PRT; 73 AA.
AC QSRCIO;
DT 01-FEB-2005 (TReMBLrel. 29, Created)
DT 01-FEB-2005 (TReMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFZp469G145.
GN Name=DKFZp469G145;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RG The German cDNA Consortium;
RA Ansoorge W., Krieger S., Regiert T., Rittmuller C., Schwager B.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR858290; CAH90527.1; -; mRNA.
DR SMR; QSRCIO; 1-73
DR GO; GO:0006464; P; protein modification; IEA.
DR InterPro; IPR000626; Ubiquitin.
DR Pfan; PF00240; ubiquitin; 1.
KW Hypothetical protein.
SQ SEQUENCE 73 AA; 8547 MW; D68BC941536AA39F CRC64;

Query Match          99.4%; Score 163; DB 2; Length 73;
Best Local Similarity 97.0%; Pred. No. 4.5e-15;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAA 33
Db 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAA 33

RESULT 7
QARSJ3_MACFA
ID QARSJ3_MACFA PRELIMINARY; PRT; 73 AA.
AC QARSJ3;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Brain cDNA, clone: Qf1A-12296, similar to human ubiquitin-like 5
DE (UBL5), (Testis cDNA, clone: Qf8A-15893, similar to human ubiquitin-
DE like 5 (UBL5)).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecidae; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA International consortium for macaque cDNA sequencing, analysis;
RT "DNA sequences of macaque genes expressed in brain or testis and its

```

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RT evolutionary implications.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
RA Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.;
RT "Substitution rate and structural divergence of 5'UTR evolution:
RT Comparative analysis between human and cynomolgus monkey cDNAs.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB169550; BAE01632.1; -; mRNA.
DR EMBL; AB168933; BAE01034.1; -; mRNA.
SQ SEQUENCE 73 AA; 8547 MW; D68BC941536AA39F CRC64;

Query Match          99.4%; Score 163; DB 2; Length 73;
Best Local Similarity 97.0%; Pred. No. 4.5e-15;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAA 33
Db 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAA 33

RESULT 8
UBL5_BRARE
ID UBL5_BRARE STANDARD; PRT; 73 AA.
AC Q7XFF2;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ubiquitin-like protein 5.
GN Name=ubl5; ORFNames=zgc:66388;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RG NIH - Zebrafish Gene Collection (ZGC) project;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Contains 1 ubiquitin-like domain.
CC -----
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CC -----
DR EMBL; BC055630; AAH5630.1; -; mRNA.
DR SMR; Q7XFF2; 1-72.
DR ZFIN; ZDB-GENE-040426-1629; zgc:66388.
DR InterPro; IPR000626; Ubiquitin.
DR Pfan; PF00240; ubiquitin; 1.
DR PROSITE; PS00299; UBIQUITIN_1; FALSE_NEG.
DR PROSITE; PS00053; UBIQUITIN_2; FALSE_NEG.
KW Ubl conjugation pathway.
FT DOMAIN 1 73 Ubiquitin-like.
SQ SEQUENCE 73 AA; 8587 MW; 23716CBB0FC7C545 CRC64;

Query Match          93.3%; Score 153; DB 1; Length 73;
Best Local Similarity 90.9%; Pred. No. 1.1e-13;
Matches 30; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAA 33
Db 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAA 33

RESULT 9
UBL5_DROME
ID UBL5_DROME STANDARD; PRT; 73 AA.
AC Q9V958; Q4QP86;

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DT 25-OCT-2004 (Rel. 45, Created)  
 DT 23-OCT-2004 (Rel. 45, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Ubiquitin-like protein 5.  
 GN Names1(2)k03203; ORFNames=CQ3450;  
 OS Drosophila melanogaster (fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=Berkley;  
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.B.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,  
 RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlike C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laekko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McIntosh M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.O.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu S.Q.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*."  
 RL Science 287:2185-2195(2000).  
 RN [2]  
 RP GENOME REANNOTATION.  
 RX MEDLINE=22426069; PubMed=12537572;  
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,  
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
 RA Bettencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,  
 RA Harris N.L., Richter J., Russo S., Schroeder A.W., Shu S.Q.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.;  
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
 RT systematic review."  
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC STRAIN=Berkley;  
 RA Stapleton M., Carlson J.W., Chavez C., Frise E., George R.A.,  
 RA Pacle J.M., Park S., Wan K.H., Yu C., Celisner S.E.;  
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -!- SIMILARITY: Contains 1 ubiquitin-like domain.

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 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 DR EMBL: AE003790; AAF57398.1; -, Genomic DNA.  
 DR EMBL: BT023690; AAY85090.1; -, mRNA.  
 DR SMR: Q9V998; 1-73.  
 DR Ensembl: CG3450; Drosophila melanogaster.  
 DR FlyBase: FBgn0022224; l(2)K03203.  
 DR GO: GO:0005737; Cytoplasm; ISS.  
 DR InterPro: IPR000826; Ubiquitin.  
 DR Pfam: PF00240; ubiquitin; 1.  
 DR PROSITE: PS00299; UBIQUITIN\_1; FALSE\_NEG.  
 DR PROSITE: PS00053; UBIQUITIN\_2; 1.  
 KW Ubl conjugation pathway. Ubiquitin-like.  
 FT DOMAIN 1 73  
 SQ SEQUENCE 73 AA; 8570 MW; 0870111AC5686A70 CRC64;  
 Query Match 92.7%; Score 152; DB 1; Length 73;  
 Best Local Similarity 87.9%; Pred. No. 1.6e-13;  
 Matches 29; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MIEVNCNRLGKKVXVKNCTDTTIGDLKKLIAA 33  
 DB 1 MIEITCNRLGKKVRVKNCPDITIGDLKKLIAA 33  
 RESULT 10  
 QSHZC1 XENLA  
 ID Q5HZC1 XENLA PRELIMINARY; PRT; 73 AA.  
 AC Q5HZC1;  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Hypothetical protein.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryo;  
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RA Richardson P.;  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 RT initiative."  
 RL Dev. Dyn. 225:384-391(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryo;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton S., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

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RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC089084; AAH89084.1; -; mRNA.
DR GO; GO:0006464; P:protein modification; IEA.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; ubiquitin; 1.
DR PROSITE; PS50053; UBIQUITIN_2; 1.
RW Hypothetical protein.
SQ SEQUENCE 73 AA; 8635 MW; 2A51E123F36FF390 CRC64;

Query Match 92.1%; Score 151; DB 2; Length 73;
Best Local Similarity 90.9%; Pred. No. 2.2e-13;
Matches 30; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAA 33
DB 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAA 33

RESULT 11
ID Q7QHM2_ANOGA PRELIMINARY; PRT; 73 AA.
AC Q7QHM2;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE ENSANGP0000015674
GN ORFNames=ENSANGG00000013185;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAA01008816; EAA05206.2; -; Genomic_DNA.
DR SMR; Q7QHM2; 1-73.
DR GO; GO:0006464; P:protein modification; IEA.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; ubiquitin; 1.
DR PROSITE; PS50053; UBIQUITIN_2; 1.
SQ SEQUENCE 73 AA; 8599 MW; 43D212BE601B3COD CRC64;

Query Match 91.5%; Score 150; DB 2; Length 73;
Best Local Similarity 84.8%; Pred. No. 3e-13;
Matches 28; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAA 33
DB 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAA 33

RESULT 12
ID Q4SMI6_TETNG PRELIMINARY; PRT; 73 AA.

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AC Q4SMI6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 18 SCAF14547, whole genome shotgun sequence.
DE (Fragment).
DE ORFNames=GSTENG00015743001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Bieumont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier S., Chappie C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01014547; CAF98146.1; -; Genomic_DNA.
FT NON TER 73
SQ SEQUENCE 73 AA; 8592 MW; 6A14CA0323F8E8EB CRC64;

Query Match 89.6%; Score 147; DB 2; Length 73;
Best Local Similarity 87.9%; Pred. No. 8e-13;
Matches 29; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAA 33
DB 1 MIEVVCNDRLGKVKVKNCPQDSIGDLKKLIAA 33

RESULT 13
ID UBL5_ARATH STANDARD; PRT; 73 AA.
AC Q9FGZ9;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ubiquitin-like protein 5.
GN Name=UBL5; OrderedLocNames=At5g42300; ORFNames=K5J14.10;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=cv. Columbia;
RX MEDLINE=20181125; PubMed=10718197;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
RT clones.";

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